

gca gag agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca 1153
 Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr
 370 375 380

 gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa 1201
 Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys
 385 390 395

 cgg gag gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata 1249
 Arg Glu Ala Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile
 400 405 410

 ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc 1297
 Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro
 415 420 425 430

 cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg 1345
 Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met
 435 440 445

 gtg ttg aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc 1393
 Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile
 450 455 460

 tcc tgg aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag 1441
 Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln
 465 470 475

 cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag 1489
 Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu
 480 485 490

 aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc 1537
 Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser

495	500	505	510
atc ctc ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc			1585
Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser			
515	520	525	
aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga			1633
Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg			
530	535	540	
gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg			1681
Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg			
545	550	555	
ggc gtg gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg			1729
Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val			
560	565	570	
ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc			1777
Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Gly Lys Leu Pro Cys			
575	580	585	590
agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc			1825
Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr			
595	600	605	
gaa ctt gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc			1873
Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly			
610	615	620	
ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga			1921
Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly			
625	630	635	
gag aaa tac atc gat ctg agg cat tagccccgaa tcacttcagc tcccttcct			1975
Glu Lys Tyr Ile Asp Leu Arg His			

640

645

gcctggacca ttcccgagtc cctgtcact cttcttcag ccaaagctca aagggactag 2035
agagaagect cctgtcccc tcgcctgcac acccccittc agagggccac tgggttagga 2095
cctgaggacc tcacttggcc ctgcaaggcc cgctttcag ggaccagtcc accaccatct 2155
cctccacgtt gagtgaagct catccaaagc aaggagcccc agictccgaa gcgggttagga 2215
gagtttcttg cagaacgtgt ttttttttta cacacattat gctgtaaata cgctcgcc 2275
gccagcagct gagctggta gcctctcga gctggttcc tgccccaaag gctggcattc 2335
caccatccag gtgcaccact gaagtgagga cacaccggag ccaggcgccct gctcatgttg 2395
aagtgcgctg ttcacacccg ctccggagag cacccagca gcatccagaa gcagctgcag 2455
tgcaagcttg catgcctgctg 1gttgtgc 2ccaccctcc 3gtctgcctct 4tcaaagtctc 2515
ctgtgacatt ttttcttgg tcagaggcca ggaactgtgt cattccttaa agatacgtgc 2575
cggggcccagg tggctcac gcctgtaaatc ccagcacttt gggaggccga ggcggcggat 2635
cacaaagtca gacgagacca tcctggctaa cacggtaaaa ccctgtctct actaaaaata 2695
caaaaaaaaaa ttagcttaggc gtagtggttg gcacclatag tccagctac tcggaaggct 2755
gaagcaggag aatggtatga atccaggagg tggagcttgc aglgagccga gaccgtgc 2815
ctgcactcca gcctggcaa cacagcgaga ctccgtctcg aggaaaaaaaaaa aaatcggt 2875
cgtagcagct ggctctgttt cgagtcaggt gaattagcct caatccccgt gttcacttgc 2935
tcccatacgcc ctcttgatgg atcacgtaaa actgaaaggc agcggggagc agacaaagat 2995
gaggtctaca ctgtccitca tggggattaa agctatggtt atattagcac caaacttcta 3055
caaaccaagc tcaggaccca accctagaag ggcccaaatg agagaatggt acttagggat 3115
ggcaaaaacgg gcctggctag agcttcgggt gtgtgtgtct gtctgtgtat gcatacatal 3175
gtgtgtatata atggtttgt caggtgtgtaa ttttgc 3235
tgtatata tataatgaaaa tatatatata tatgaaaaat aaagcttaat tgtccca 3295

<210> 96

211 <211> 646

<212> PRT

<213> Homo sapiens

<400> 96

Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Leu Ala Ala Cys Cys
1 5 10 15
Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala
20 25 30
Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys
35 40 45
Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser
50 55 60
Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln
65 70 75 80
Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp
85 90 95
Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg
100 105 110
Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile
115 120 125
Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn
130 135 140
Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr
145 150 155 160
Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys
165 170 175
Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser
180 185 190

Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
195 200 205
Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
210 215 220
Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
225 230 235 240
Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
245 250 255
Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
260 265 270
Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn
275 280 285
Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val
290 295 300
Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys
305 310 315 320
Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln
325 330 335
Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
340 345 350
Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
355 360 365
Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln
370 375 380
Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu
385 390 395 400
Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly

405 410 415
Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp
420 425 430
Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu
435 440 445
Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp
450 455 460
Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val
465 470 475 480
Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly
485 490 495
Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu
500 505 510
Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr
515 520 525
Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn
530 535 540
Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val
545 550 555 560
Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly
565 570 575
Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg
580 585 590
Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu
595 600 605
Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu

610 615 620

Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys
 625 630 635 640
 Tyr Ile Asp Leu Arg His

645

<210> 97

<211> 1642

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (158)..(1279)

<400> 97

gaatcgccgg tccgcaggc cccggatgtt gcggacagta tgaggcaagc gcagggggac 60
 ggggaccaggc agctgtcgcc gccgcctcta gggtgaagag ggaacagaaaa tccttgcccc 120
 ctgactttgg aaatctcgtt taacctcaa actggcg atg tca agg gtt cca agt 175

Met Ser Arg Val Pro Ser

1 5

cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223
 .Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp

10 15 20

tgc lac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc 271

Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile

25 30 35

aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt 319

Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser

40	45	50	
tct aca ttt tca tca gga gca aat gat aaa ctg aaa tgg tgt ttg cga 367			
Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg			
55	60	65	70
gta aac ccc aaa ggg tta gat gaa gaa agc aaa gat tac ctg tca ctt 415			
Val Asn Pro Lys Gly Leu Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu			
75	80	85	
tac ctg tta ctg gtc agc tgt cca aag agt gaa gtt cggt gca aaa ttc 463			
Tyr Leu Leu Val Ser Cys Pro Lys Ser Glu Val Arg Ala Lys Phe			
90	95	100	
aaa ttc tcc atc ctg aat gcc aag gga gaa gaa acc aaa gct atg gag 511			
Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu			
105	110	115	
agt caa cgg gca tat agg ttt gtg caa ggc aaa gac tgg gga ttc aag 559			
Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly Lys Asp Trp Gly Phe Lys			
120	125	130	
aaa ttc atc cgt aga gat ttt ctt ttg gat gag gcc aac ggg ctt ctc 607			
Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu			
135	140	145	150
cct gat gac aag ctt acc ctc ttc tgc gag gtg agt gtt gtg caa gat 655			
Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu Val Ser Val Val Gln Asp			
155	160	165	
tct gtc aac att tct ggc cag aat acc atg aac atg gta aag gtt cct 703			
Ser Val Asn Ile Ser Gly Gln Asn Thr Met Asn Met Val Lys Val Pro			
170	175	180	
gag tgc cgg ctg gca gat gag tta gga gga ctg tgg gag aat tcc cgg 751			
Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly Leu Trp Glu Asn Ser Arg			

185	190	195	
ttc aca gac tgc tgc ttg tgt gtc gcc ggc cag gaa ttc cag gct cac 799			
Phe Thr Asp Cys Cys Leu Cys Val Ala Gly Gln Glu Phe Gln Ala His			
200	205	210	
aag gct atc tta gca gct cgt tct ccg gtt ttt agt gcc atg ttt gaa 847			
Lys Ala Ile Leu Ala Ala Arg Ser Pro Val Phe Ser Ala Met Phe Glu			
215	220	225	230
cat gaa atg gag gag agc aaa aag aat cga gtt gaa atc aat gat gtg 895			
His Glu Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Val			
235	240	245	
gag cct gaa gtt ttt aag gaa atg atg tgc ttc att tac acg ggg aag 943			
Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys			
250	255	260	
gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac 991			
Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Ala Asp			
265	270	275	
aag tat gcc ctg gag cgc tta aag gtc atg tgt gag gat gcc ctc tgc 1039			
Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys			
280	285	290	
agt aac ctg tcc gtg gag aac gct gca gaa att ctc atc ctg gcc gac 1087			
Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp			
295	300	305	310
ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac 1135			
Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn			
315	320	325	
tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg 1183			

Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val

330 335 340

gtg tca cat ccc cac ttg gtg gct gag gca tac cgc tct ctg gct tca 1231

Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser

345 350 355

gca cag tgc cct ttt ctg gga ccc cca cgc aaa cgc ctg aag caa tcc 1279

Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg Lys Arg Leu Lys Gln Ser

360 365 370

taagatcccg cttgttgtaa gactccgttt aatttcaga agcagcagcc actgttgctg 1339

ccactgacca ccaggttagac agcgcaatct gggagctt tactctgttg tgagggaaag 1399

agactgcatt gtggccccag acttttaaaa cagcacta aa taacttgggg gaaacggggg 1459

gagggaaaat gaaatgaaaa ccctgttgct gcgtcactgt gttcccttgc gcctgtctga 1519

gttigatact gtggggatc agtttaggcg ctggcccgag gatatcccag cggtggtaact 1579

tccgagacac ctgtctgcat ctgactgagc agaacaatc gtcaggcc 1639

agg 1642

<210> 98

<211> 374

<212> PRT

<213> Homo sapiens

<400> 98

Met Ser Arg Val Pro Ser Pro Pro Pro Ala Glu Met Ser Ser Gly

1 5 10 15

Pro Val Ala Glu Ser Trp Cys Tyr Thr Gln Ile Lys Val Val Lys Phe

20 25 30

Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met

35 40 45

Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys
50 55 60
Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser
65 70 75 80
Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Val Ser Cys Pro Lys Ser
85 90 95
Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu
100 105 110
Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly
115 120 125
Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
130 135 140
Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu
145 150 155 160
Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met
165 170 175
Asn Met Val Lys Val Pro Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly
180 185 190
Leu Trp Glu Asn Ser Arg Phe Thr Asp Cys Cys Leu Cys Val Ala Gly
195 200 205
Gln Glu Phe Gln Ala His Lys Ala Ile Leu Ala Ala Arg Ser Pro Val
210 215 220
Phe Ser Ala Met Phe Glu His Glu Met Glu Glu Ser Lys Lys Asn Arg
225 230 235 240
Val Glu Ile Asn Asp Val Glu Pro Glu Val Phe Lys Glu Met Met Cys
245 250 255
Phe Ile Tyr Thr Gly Lys Ala Pro Asn Leu Asp Lys Met Ala Asp Asp

260 265 270
Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met
275 280 285
Cys Glu Asp Ala Leu Cys Ser Asn Leu Ser Val Glu Asn Ala Ala Glu
290 295 300
Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln
305 310 315 320
Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser
325 330 335
Gly Trp Lys Ser Met Val Val Ser His Pro His Leu Val Ala Glu Ala
340 345 350
Tyr Arg Ser Leu Ala Ser Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg
355 360 365
Lys Arg Leu Lys Gln Ser
370

<210> 99

<211> 5722

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (112)..(3621)

<400> 99

ggacgcacag gcattccccg cgcccttcca gcccgcgg ccctgccac cgtccccgc 60

cgccgcgctc cggtacacac aggatccctg ctgggcacca acagtcacac c atg ggg 117

Met Gly

1

ctg gcc tgg gga cta ggc gtc ctg ttc ctg atg cat gtg tgt ggc acc 165
Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys Gly Thr
5 10 15
aac cgc att cca gag tct ggc gga gac aac agc gtg ttt gac atc ttt 213
Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp Ile Phe
20 25 30
gaa ctc acc ggg gcc gcc cgc aag ggg tct ggg cgc cga ctg gtg aag 261
Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu Val Lys
35 40 45 50
ggc ccc gac cct tcc agc cca gct ttc cgc atc gag gat gcc aac ctg 309
Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala Asn Leu
55 60 65
atc ccc cct gtg cct gat gac aag ttc caa gac ctg gtg gat gct gtg 357
Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp Ala Val
70 75 80
cgg gca gaa aag ggt ttc ctc ctt ctg gca tcc ctg agg cag atg aag 405
Arg Ala Glu Lys Gly Phe Leu Leu Ala Ser Leu Arg Gln Met Lys
85 90 95
aag acc cgg ggc acg ctg ctg gcc ctg gag cgg aaa gac cac tct ggc 453
Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His Ser Gly
100 105 110
cag gtc ttc agc gtg gtg tcc aat ggc aag gcg ggc acc ctg gac ctc 501
Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu Asp Leu
115 120 125 130
agc ctg acc gtc caa gga aag cag cac gtc gtg tct gtg gaa gaa gct 549

Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu Glu Ala
 135 140 145
 ctc ctg gca acc ggc cag tgg aag agc atc acc ctg ttt gtg cag gaa 597
 Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val Gln Glu
 150 155 160
 gac agg gcc cag ctg tac atc gac tgt gaa aag atg gag aat gct gag 645
 Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn Ala Glu
 165 170 175
 ttg gac gtc ccc atc caa agc gtc ttc acc aga gac ctg gcc agc atc 693
 Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala Ser Ile
 180 185 190
 gcc aga ctc cgc atc gca aag ggg ggc gtc aat gac aat ttc cag ggg 741
 Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe Gln Gly
 195 200 205 210
 gtg ctg cag aat gtg agg ttt gtc ttt gga acc aca cca gaa gac atc 789
 Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu Asp Ile
 215 220 225
 ctc agg aac aaa ggc tgc tcc agc tct acc agt gtc ctc ctc acc ctt 837
 Leu Arg Asn Lys Gly Cys Ser Ser Thr Ser Val Leu Leu Thr Leu
 230 235 240
 gac aac aac gtg gtg aat ggt tcc agc cct gcc atc cgc act aac tac 885
 Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr Asn Tyr
 245 250 255
 att ggc cac aag aca aag gac ttg caa gcc atc tgc ggc atc tcc tgt 933
 Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile Ser Cys
 260 265 270
 gat gag ctg tcc agc atg gtc ctg gaa ctc agg ggc ctg cgc acc att 981

Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg Thr Ile
275 280 285 290
gtg acc acg ctg cag gac agc atc cgc aaa gtg act gaa gag aac aaa 1029
Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu Asn Lys
295 300 305
gag ttg gcc aat gag ctg agg cgg cct ccc cta tgc tat cac aac gga 1077
Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly
310 315 320
gtt cag tac aga aat aac gag gaa tgg act gtt gat agc tgc act gag 1125
Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys Thr Glu
325 330 335
tgt cac tgt cag aac tca gtt acc atc tgc aaa aag gtg tcc tgc ccc 1173
Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser Cys Pro
340 345 350
atc atg ccc tgc tcc aat gcc aca gtt cct gat gga gaa tgc tgt cct 1221
Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys Cys Pro
355 360 365 370
cgc tgt tgg ccc agc gac tct gcg gac gat ggc tgg tct cca tgg tcc 1269
Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro Trp Ser
375 380 385
gag tgg acc tcc tgt tct acg agc tgt ggc aat gga att cag cag cgc 1317
Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln Gln Arg
390 395 400
ggc cgc tcc tgc gat agc ctc aac aac cga tgt gag ggc tcc tcg gtc 1365
Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser Ser Val
405 410 415

cag aca cgg acc tgc cac att cag gag tgt gac aaa aga ttt aaa cag 1413
 Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe Lys Gln
 420 425 430

gat ggt ggc tgg agc cac tgg tcc ccg tgg tca tct tgt tct gtg aca 1461
 Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr
 435 440 445 450

tgt ggt gat ggt gtg atc aca agg atc cgg ctc tgc aac tct ccc agc 1509
 Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser
 455 460 465

ccc cag atg aat ggg aaa ccc tgt gaa ggc gaa gcg cgg gag acc aaa 1557
 Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys
 470 475 480

gcc tgc aag aaa gac gcc tgc ccc atc aat gga ggc tgg ggt cct tgg 1605
 Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly Pro Trp
 485 490 495

tca cca tgg gac atc tgt tct gtc acc tgt gga gga ggg gta cag aaa 1653
 Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Val Gln Lys
 500 505 510

cgt agt cgt ctc tgc aac aac ccc gca ccc cag ttt gga ggc aag gac 1701
 Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly Lys Asp
 515 520 525 530

tgc gtt ggt gat gta aca gaa aac cag atc tgc aac aag cag gac tgt 1749
 Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln Asp Cys
 535 540 545

cca att gat gga tgc ctg tcc aat ccc tgc ttt gcc ggc gtg aag tgt 1797
 Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val Lys Cys
 550 555 560

act	agc	tac	cct	gat	ggc	agc	tgg	aaa	tgt	ggt	gct	tgt	ccc	cct	ggt		1845
Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro Pro Gly																	
565			570						575								
tac agt gga aat ggc atc cag tgc aca gat gtt gat gag tgc aaa gaa															1893		
Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys Lys Glu																	
580			585						590								
gtg cct gat gcc tgc ttc aac cac aat gga gag cac cgg tgt gag aac															1941		
Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys Glu Asn																	
595			600			605			610								
acg gac ccc ggc tac aac tgc ctg ccc tgc ccc cca cgc ttc acc ggc															1989		
Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe Thr Gly																	
615			620			625											
tca cag ccc ttc ggc cag ggt gtc gaa cat gcc acg gcc aac aaa cag															2037		
Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn Lys Gln																	
630			635			640											
gtg tgc aag ccc cgt aac ccc tgc acg gal ggg acc cac gac tgc aac															2085		
Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn																	
645			650			655											
aag aac gcc aag tgc aac tac ctg ggc cac tat agc gac ccc atg tac															2133		
Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro Met Tyr																	
660			665			670											
cgc tgc gag tgc aag cct ggc tac gct ggc aat ggc atc atc tgc ggg															2181		
Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile Cys Gly																	
675			680			685			690								
gag gac aca gac ctg gat ggc tgg ccc aat gag aac ctg gtg tgc gtg															2229		
Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val Cys Val																	

695	700	705	
gcc aat gcg act tac cac tgc aaa aag gat aat tgc ccc aac ctt ccc			2277
Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn Leu Pro			
710	715	720	
aac tca ggg cag gaa gac tat gac aag gat gga att ggt gat gcc tgt			2325
Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp Ala Cys			
725	730	735	
gat gat gac gat gac aat gat aaa att cca gat gac agg gac aac tgt			2373
Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp Asn Cys			
740	745	750	
cca ttc cat tac aac cca gct cag tat gac tat gac aga gat gat gtg			2421
Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp Asp Val			
755	760	765	770
gga gac cgc tgt gac aac tgt ccc tac aac cac aac cca gat cag gca			2469
Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp Gln Ala			
775	780	785	
gac aca gac aac aat ggg gaa gga gac gcc tgt gct gca gac att gat			2517
Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp			
790	795	800	
gga gac ggt atc ctc aat gaa cgg gac aac tgc cag tac gtc tac aat			2565
Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn			
805	810	815	
tgt gac cag aga gac act gat atg gat ggg gtt gga gat cag tgt gac			2613
Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp			
820	825	830	
aat tgc ccc ttt gaa cac aat ccg gat cag ctg gac tct gac tca gac			2661
Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp			

835	840	845	850	
cgc att gga gat acc tgt gac aac aat cag gat att gat gaa gat ggc				2709
Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly				
855		860		865
cac cag aac aat ctg gac aac tgt ccc tat gtg ccc aat gcc aac cag				2757
His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln				
870		875		880
gct gac cat gac aaa gat ggc aag gga gat gcc tgt gac cac gat gat				2805
Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp				
885		890		895
gac aac gat ggc att cct gat gac aag gac aac tgc aga ctc gtg ccc				2853
Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu Val Pro				
900		905		910
aat ccc gac cag aag gac tct gac ggc gat ggt cga ggt gat gcc tgc				2901
Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp Ala Cys				
915		920		925
aaa gat gat ttt gac cat gac agt gtg cca gac atc gat gac atc tgt				2949
Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp Ile Cys				
935		940		945
cct gag aat gtt gac atc agt gag acc gat ttc cgc cga ttc cag atg				2997
Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe Gln Met				
950		955		960
att cct ctg gac ccc aaa ggg aca tcc caa aat gac cct aac tgg gtt				3045
Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn Trp Val				
965		970		975
gta cgc cat cag ggt aaa gaa ctc gtc cag act gtc aac tgt gat cct				3093

Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys Asp Pro
 980 985 990
 gga ctc gct gta ggt tat gat gag ttt aat gct gtg gac ttc agt ggc 3141
 Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe Ser Gly
 995 1000 1005 1010
 acc ttc ttc alc aac acc gaa agg gac gat gac tat gct gga ttt gtc 3189
 Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly Phe Val
 1015 1020 1025
 ttt ggc tac cag tcc agc agc cgc ttt tat gtt gtg atg tgg aag caa 3237
 Phe Gly Tyr Gln Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln
 1030 1035 1040
 gtc acc cag tcc tac tgg gac acc aac ccc acg agg gct cag gga tac 3285
 Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln Gly Tyr
 1045 1050 1055
 tcg ggc ctt tct gtg aaa gtt gta aac tcc acc aca ggg cct ggc gag 3333
 Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro Gly Glu
 1060 1065 1070
 cac ctg cgg aac gcc ctg tgg cac aca gga aac acc cct ggc cag gtg 3381
 His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val
 1075 1080 1085 1090
 cgc acc ctg tgg cat gac cct cgt cac ata ggc tgg aaa gat ttc acc 3429
 Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp Phe Thr
 1095 1100 1105
 gcc tac aga tgg cgt ctc agc cac agg cca aag acg ggt ttc att aga 3477
 Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg
 1110 1115 1120
 gtg gtg atg tat gaa ggg aag aaa atc atg gct gac tca gga ccc atc 3525

Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly Pro Ile
1125 1130 1135
tat gat aaa acc tat gct ggt ggt aga cta ggg ttg ttt gtc ttc tct 3573
Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser
1140 1145 1150
caa gaa atg gtg ttc ttc tct gac ctg aaa tac gaa tgt aga gat ccc 3621
Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Pro
1155 1160 1165 1170
taatcatcaa atttgtgatt gaaagactga tcataaacca atgctggat tgcacccct 3681
ggaactatgg gcttgagaaa acccccagga tcacttctcc ttggcttcct tccttcgt 3741
gcttgcatca gtgtggactc ctagaacgtg cgacctgcct caagaaaatg cagtttcaa 3801
aaacagactc atcagcattc agcctccaat gaataagaca tctccaagg atataaaca 3861
ttgccttggt tccctttga aaaagcatct acttgcitca gttggaaagg tgcccatcc 3921
actctgcctt tgcacagag cagggtgcta ttgtgaggcc atctctgagc agtggactca 3981
aaagcatttt cagggatgtc agagaaggga ggactcacta gaattagcaa acaaaaccac 4041
cctgacatcc tccttcagga acacggggag cagaggccaa agcactaagg ggagggcgca 4101
tacccgagac gattgtatga agaaaaatg gaggaactgt tacatgttcg gtactaagtc 4161
atttcaggg gattgaaaga ctattgctgg atttcatgtat gctgactggc gtttagctgtat 4221
taacccatgt aaataggcac ttaaatagaa gcagggaaagg gagacaaaga ctggcttcg 4281
gacttcctcc ctgatccccca cccttactca tcaccttgca gtggccagaa ttaggaaatc 4341
agaatcaaac cagtgttaagg cagtgctggc tgccattgcc tggcacatt gaaattggtg 4401
gcitcattct agatgtatgt tgcacatgt tagcaggaaa atagaaaaac ctaccatctc 4461
agtggcacc agctgcctcc caaaggaggg gcagccgtgc ttatattttt atggttacaa 4521
tggcacaaaa ttattatcaa cctaactaaa acattccctt tctctttttt ccgtattac 4581
taggttagttt tctaaattctc tctttggaa gtatgattt tttaaagtct ttacgtatgt 4641
aaatattttat ttttactta ttctggaaaga tctggctgaa ggattattca tggaacagga 4701

〈210〉 100

<211> 1170

<212> PRT

<213> Homo sapiens

<400> 100

Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys

1 5 10 15

Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp

	20	25	30
Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu			
	35	40	45
Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala			
	50	55	60
Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp			
	65	70	75
Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln			
	85	90	95
Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His			
	100	105	110
Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu			
	115	120	125
Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu			
	130	135	140
Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val			
	145	150	155
Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn			
	165	170	175
Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala			
	180	185	190
Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe			
	195	200	205
Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu			
	210	215	220
Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu			
	225	230	235
			240

Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
245 250 255
Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
260 265 270
Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
275 280 285
Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
290 295 300
Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
305 310 315 320
Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
325 330 335
Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser
340 345 350
Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys
355 360 365
Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro
370 375 380
Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln
385 390 395 400
Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
405 410 415
Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe
420 425 430
Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser
435 440 445

Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser
450 455 460

Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
465 470 475 480

Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly
485 490 495

Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
500 505 510

Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly
515 520 525

Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln
530 535 540

Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val
545 550 555 560

Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro
565 570 575

Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys
580 585 590

Lys Glu Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys
595 600 605

Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe
610 615 620

Thr Gly Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn
625 630 635 640

Lys Gln Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp
645 650 655

Cys Asn Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro

660 665 670
Met Tyr Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile
675 680 685
Cys Gly Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val
690 695 700
Cys Val Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn
705 710 715 720
Leu Pro Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp
725 730 735
Ala Cys Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp
740 745 750
Asn Cys Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp
755 760 765
Asp Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp
770 775 780
Gln Ala Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp
785 790 795 800
Ile Asp Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val
805 810 815
Tyr Asn Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln
820 825 830
Cys Asp Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp
835 840 845
Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu
850 855 860
Asp Gly His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala

865 870 875 880
Asn Gln Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His
885 890 895
Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp Lys Asn Cys Arg Leu
900 905 910
Val Pro Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Arg Gly Asp
915 920 925
Ala Cys Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp
930 935 940
Ile Cys Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe
945 950 955 960
Gln Met Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn
965 970 975
Trp Val Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys
980 985 990
Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe
995 1000 1005
Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Tyr Ala Gly
1010 1015 1020
Phe Val Phe Gly Tyr Gln Ser Ser Arg Phe Tyr Val Val Met Trp
1025 1030 1035 1040
Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln
1045 1050 1055
Gly Tyr Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro
1060 1065 1070
Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly
1075 1080 1085

Gln Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp
1090 1095 1100
Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe
1105 1110 1115 1120
Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly
1125 1130 1135
Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val
1140 1145 1150
Phe Ser Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg
1155 1160 1165
Asp Pro
1170

<210> 101

<211> 838

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (35)..(568)

<400> 101

gaattccgga gtttcatcc agccacgggc cagc atg tct ggg ggc aaa tac gta 55

Met Ser Gly Gly Lys Tyr Val

1 5

gac tcg gag gga cat ctc tac acc gtt ccc atc cg^g gaa cag ggc aac 103

Asp Ser Glu Gly His Leu Tyr Thr Val Pro Ile Arg Glu Gln Gly Asn

10 15 20

atc tac aag ccc aac aac aag gcc atg gca gac gag ctg agc gag aag	151		
Ile Tyr Lys Pro Asn Asn Lys Ala Met Ala Asp Glu Leu Ser Glu Lys			
25	30	35	
caa gtg tac gac gcg cac acc aag gag atc gac ctg gtc aac cgc gac	199		
Gln Val Tyr Asp Ala His Thr Lys Glu Ile Asp Leu Val Asn Arg Asp			
40	45	50	55
cct aaa cac ctc aac gat gac gtg gtc aag att gac ttt gaa gat gtg	247		
Pro Lys His Leu Asn Asp Asp Val Val Lys Ile Asp Phe Glu Asp Val			
60	65	70	
att gca gaa cca gaa ggg aca cac agt ttt cac ggc att tgg aag gcc	295		
Ile Ala Glu Pro Glu Gly Thr His Ser Phe His Gly Ile Trp Lys Ala			
75	80	85	
agc ttc acc acc ttc act gtg acg aaa tac tgg ttt tac cgc ttg ctg	343		
Ser Phe Thr Thr Phe Thr Val Thr Lys Tyr Trp Phe Tyr Arg Leu Leu			
90	95	100	
tct gcc ctc ttt ggc atc ccg atg gca ctc atc tgg ggc att tac ttc	391		
Ser Ala Leu Phe Gly Ile Pro Met Ala Leu Ile Trp Gly Ile Tyr Phe			
105	110	115	
gcc att ctc tct ttc ctg cac atc tgg gca gtt gta cca tgc att aag	439		
Ala Ile Leu Ser Phe Leu His Ile Trp Ala Val Val Pro Cys Ile Lys			
120	125	130	135
agc ttc ctg att gag att cag tgc acc agc cgt gtc tat tcc atc tac	487		
Ser Phe Leu Ile Glu Ile Gln Cys Thr Ser Arg Val Tyr Ser Ile Tyr			
140	145	150	
gtc cac acc gtc tgt gac cca ctc ttt gaa gct gtt ggg aaa ata ttc	535		
Val His Thr Val Cys Asp Pro Leu Phe Glu Ala Val Gly Lys Ile Phe			

155

160

165

agc aat gtc cgc atc aac ttg cag aaa gaa ata taaatgacat ttcaaggata 588

Ser Asn Val Arg Ile Asn Leu Gln Lys Glu Ile

170

175

gaagtataacc tgatttttt tccttttaat ttccctggtg ccaattcaa gttccaagtt 648

gctaatacag caacgaattt atgaattgaa ttatcttgt tgaaaataaa aagatcactt 708

tctcagttt cataagtatt atgtctttc tgagctattt catctattt tggcagtcg 768

aattttaaa acccatttat atttcttcc ttacctttt atttgcatgt ggtcaacca 828

tcgcatttatt

838

<210> 102

<211> 178

<212> PRT

<213> Homo sapiens

<400> 102

Met Ser Gly Gly Lys Tyr Val Asp Ser Glu Gly His Leu Tyr Thr Val

1

5

10

15

Pro Ile Arg Glu Gln Gly Asn Ile Tyr Lys Pro Asn Asn Lys Ala Met

20

25

30

Ala Asp Glu Leu Ser Glu Lys Gln Val Tyr Asp Ala His Thr Lys Glu

35

40

45

Ile Asp Leu Val Asn Arg Asp Pro Lys His Leu Asn Asp Asp Val Val

50

55

60

Lys Ile Asp Phe Glu Asp Val Ile Ala Glu Pro Glu Gly Thr His Ser

65

70

75

80

Phe His Gly Ile Trp Lys Ala Ser Phe Thr Thr Phe Thr Val Thr Lys

85

90

95

Tyr Trp Phe Tyr Arg Leu Leu Ser Ala Leu Phe Gly Ile Pro Met Ala

100 105 110

Leu Ile Trp Gly Ile Tyr Phe Ala Ile Leu Ser Phe Leu His Ile Trp

115 120 125

Ala Val Val Pro Cys Ile Lys Ser Phe Leu Ile Glu Ile Gln Cys Thr

130 135 140

Ser Arg Val Tyr Ser Ile Tyr Val His Thr Val Cys Asp Pro Leu Phe

145 150 155 160

Glu Ala Val Gly Lys Ile Phe Ser Asn Val Arg Ile Asn Leu Gln Lys

165 170 175

Glu Ile

<210> 103

<211> 2269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(444)

<400> 103

ccg ccc gcc acc agc tac gcc ccg tcc gac gtg ccc tcg ggg gtc gcg 48

Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala

1 5 10 15

ctg ttc ctc acc atc cct ttc gcc ttc ttc ctg ccc gag ctg ata ttt 96

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20 25 30

ggg ttc ttg gtc tgg acc atg gta gcc gcc acc cac ata gta tac ccc 144

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro

35

40

45

ttg ctg caa gga tgg gtg atg tat gtc tcg ctc acc tcg ttt ctc atc 192

Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile

50

55

60

tcc ttg atg ttc ctg ttg tct tac ttg ttt gga ttt tac aaa aga ttt 240

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe

65

70

75

80

gaa tcc tgg aga gtt ctg gac agc ctg tac cac ggg acc act ggc atc 288

Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile

85

90

95

ctg tac atg agc gct gcc gtc cta caa gta cat gcc acg att gtt tct 336

Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser

100

105

110

gag aaa ctg ctg gac cca aga att tac tac att aat tcg gca gcc tcg 384

Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser

115

120

125

ttc ttc gcc ttc atc gcc acg ctg ctc tac att ctc cat gcc ttc agc 432

Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser

130

135

140

atc tat tac cac tcatgtcacatcgccgcgcaggcc aaggggggaaa tgctcttgc 484

Ile Tyr Tyr His

145

aagctccaat tatttgtccc caaaaggcagc tcccaacgtt tgccatctgg atgacaaacg 544

gaagatccac taaaacgtcc acgggattaa cagaacgtcc ttgcagactg agcgatgaca 604

ccacactttg ttggacatt taaattcact ctgctgaata ggaggaagct ttcttttc 664

ctggaaaaac aactgtctct tggattatc tgaccatgaa cttgtcttc tagacaactc 724

acatcaaaggccacttcca ctaatggaga atccttagccc cactaatggcc aagtctgttt 784
ggggattttg cctcagctat gggcttcctt agagtaggtc taggggaata ctcagtcgtt 844
tctttttt gtttgtttt tttttttt tttagacgg agtctcgctc ttccctcaag 904
gctggagtgc agtgacgcga tcctccactca ctgcaggctc cgccctccgg gtccccgcca 964
ttctccctgcc tcagccccc gagtagccgg gactacaggg gccaccaccat atgcccggct 1024
aatttagttt tatttttagt agagatgggg ttccaccgtt ttagccagga tggtctcgat 1084
ctcctgacct cgtgatccgc ccgcctcgcc ctccaaagt gctgggatata caggcgttag 1144
ccaccgtgcc cggcctgatt ctctaaaat tgaagaggtt ctgcctaggc cttcagatct 1204
aacgcagatg catagaccctt gtccctggta ctgttcagc ctgtgttggg gagccgttgt 1264
cccgagttcc ctgggaggct gacagggtca agccaccctt cccaccaccc tccacttcc 1324
cctcccccattt cctctccagc attaggattt aaggaaatc tgcatgaagc caatttttag 1384
ggtagacgtt tggggaaaat aaatcattttt acagtaagac ctggggcttg aggggtgggg 1444
aaaggggagg gaagggcata gcctgcttcc ccatgagtct gacatctggg aaactgagca 1504
gctgcccggac gcctgggtca ggaatccaag accccaccc ttaaggactt gttccctcaga 1564
aagcacccctc agggaaaaag gtgaaaacat tacatccgtt gatttccctt ccacaaccgc 1624
atttggaaagaa aaggctgccc caacatctca gcgaggagttt aaggaccat gtccctggaa 1684
ccgcgcgtgc ccacctgcac tcacccccc cacattctt taaggacccg gtggccctcc 1744
gaggctggcg gaatgggtttt gcccacgggg ttggcaagg gtcaccagg acctaaccgg 1804
gcaaaagtgtt gcacactaaa atatcaaattt aagggtgtttt gttttaaagt aaatgttttt 1864
ctaaagaaag ctgtgttctt ctgttgaccc agacgaatag ggcacagccc tgtaactgca 1924
cgtgccttctt gtcattggga atgaaataaa ttattacgag aaaggactt gtccttaactt 1984
gtttgaggcc ttacagttttt gtatctacat ttcccttc ctgggtttt cggggacagg 2044
gacagaacta caggagtcat gggaaagaaa attctggctt cactactgtt cactgctcac 2104
tttctgtatca ctctgtatctt ttttttttt tttttttt gcaacctgtt accttgaaaa 2164
gcttctatgtt gtccttcctt ttgttgccctt gcagctgtttt aggtatgtca ctgattacta 2224
tttacttaatgtt agccacatgc aaataaaaatgttggtaa aatgg 2269

<210> 104

<211> 148

<212> PRT

<213> Homo sapiens

<400> 104

Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala

1

5

10

15

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20

25

30

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro

35

40

45

Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile

50

55

60

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe

65

70

75

80

Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile

85

90

95

Ile Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser

100

105

110

Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser

115

120

125

Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser

130

135

140

Ile Tyr Tyr His

145

<210> 105

<211> 2899

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(2196)

<400> 105

gatctgaatt cggccccagg tagagctcca ggcggccgtc aggccccact cgaccctctc 60

gggcctcgcc tacttggact gcggcgaaat atg gcg gct ccg atg act ccc gcg 114

Met Ala Ala Pro Met Thr Pro Ala

1 5

gct cgg ccc gag gac tac gag gcg gcg ctg aat gcc gcc ctg gct gac 162

Ala Arg Pro Glu Asp Tyr Glu Ala Ala Leu Asn Ala Ala Leu Ala Asp

10 15 20

gtg ccc gaa ctg gcc aga ctg ctg gag atc gac ccg tac ttg aag ccc 210

Val Pro Glu Leu Ala Arg Leu Leu Glu Ile Asp Pro Tyr Leu Lys Pro

25 30 35 40

tac gcc gtg gac ttc cag cgc agg tat aag cag ttt agc caa att ttg 258

Tyr Ala Val Asp Phe Gln Arg Arg Tyr Lys Gln Phe Ser Gln Ile Leu

45 50 55

aag aac att gga gaa aat gaa ggt ggt att gat aag ttt tcc aga ggc 306

Lys Asn Ile Gly Glu Asn Glu Gly Ile Asp Lys Phe Ser Arg Gly

60 65 70

tat gaa tca ttt ggc gtc cac aga tgt gct gat ggt ggt tta tac tcc 354

Tyr Glu Ser Phe Gly Val His Arg Cys Ala Asp Gly Gly Leu Tyr Ser

75 80 85

aaa gaa tgg gcc ccg gga gca gaa gga gtt ttt ctt act gga gat ttt 402
 Lys Glu Trp Ala Pro Gly Ala Glu Gly Val Phe Leu Thr Gly Asp Phe
 90 95 100

 aat ggt tgg aat cca ttt tcg tac cca tac aaa aaa ctg gat tat gga 450
 Asn Gly Trp Asn Pro Phe Ser Tyr Pro Tyr Lys Lys Leu Asp Tyr Gly
 105 110 115 120

 aaa tgg gag ctg tat atc cca cca aag cag aat aaa tct gta ctc gtg 498
 Lys Trp Glu Leu Tyr Ile Pro Pro Lys Gln Asn Lys Ser Val Leu Val
 125 130 135

 cct cat gga tcc aaa tta aag gta gtt att act agt aaa agc gga gag 546
 Pro His Gly Ser Lys Leu Lys Val Val Ile Thr Ser Lys Ser Gly Glu
 140 145 150

 atc ttg tat cgt att tca ccg tgg gca aag tat gtg gtt cgt gaa ggt 594
 Ile Leu Tyr Arg Ile Ser Pro Trp Ala Lys Tyr Val Val Arg Glu Gly
 155 160 165

 gat aat gtg aat tat gat tgg ata cac tgg gat cca gaa cac tca tat 642
 Asp Asn Val Asn Tyr Asp Trp Ile His Trp Asp Pro Glu His Ser Tyr
 170 175 180

 gag ttt aag cat tcc aga cca aag aag cca cgg agt cta aga att tat 690
 Glu Phe Lys His Ser Arg Pro Lys Lys Pro Arg Ser Leu Arg Ile Tyr
 185 190 195 200

 gaa tct cat gtg gga att tct tcc cat gaa gga aaa gta gct tct tat 738
 Glu Ser His Val Gly Ile Ser Ser His Glu Gly Lys Val Ala Ser Tyr
 205 210 215

 aaa cat ttt aca tgc aat gta cta cca aga atc aaa ggc ctt gga tac 786
 Lys His Phe Thr Cys Asn Val Leu Pro Arg Ile Lys Gly Leu Gly Tyr
 220 225 230

aac tgc att cag ttg atg gca atc atg gag cat gct tac tat gcc agc	834		
Asn Cys Ile Gln Leu Met Ala Ile Met Glu His Ala Tyr Tyr Ala Ser			
235	240	245	
ttt ggt tac caa atc aca agc ttc ttt gca gct tcc agc cgt tat gga		882	
Phe Gly Tyr Gln Ile Thr Ser Phe Phe Ala Ala Ser Ser Arg Tyr Gly			
250	255	260	
aca cct gaa gag cta caa gaa ctg gta gac aca gct cat tcc atg ggt		930	
Thr Pro Glu Glu Leu Gln Glu Leu Val Asp Thr Ala His Ser Met Gly			
265	270	275	280
atc ata gtc ctc tta gat gtg gta cac agc cat gct tca aaa aat tca		978	
Ile Ile Val Leu Leu Asp Val Val His Ser His Ala Ser Lys Asn Ser			
285	290	295	
gca gat gga ttg aat atg ttt gat ggg aca gat tcc tgt tat ttt cat		1026	
Ala Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe His			
300	305	310	
tct gga cct aga ggg act cat gat ctt tgg gat agc aga ttg ttt gcc		1074	
Ser Gly Pro Arg Gly Thr His Asp Leu Trp Asp Ser Arg Leu Phe Ala			
315	320	325	
tac tcc agc tgg gaa gtt tta aga ttc ctt ctg tca aac ata aga tgg		1122	
Tyr Ser Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ile Arg Trp			
330	335	340	
tgg ttg gaa gaa tat cgc ttt gat gga ttt cgt ttt gat ggt gtt acg		1170	
Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr			
345	350	355	360
tcc atg ctt tat cat cac cat gga gtg ggt caa ggt ttc tca ggt gat		1218	
Ser Met Leu Tyr His His Gly Val Gly Gln Gly Phe Ser Gly Asp			

365	370	375	
tac agt gaa tat ttc gga cta caa gta gat gaa gat gcc ttg act tac 1266			
Tyr Ser Glu Tyr Phe Gly Leu Gln Val Asp Glu Asp Ala Leu Thr Tyr			
380	385	390	
ctc atg ttg gca aat cat ttg gtt cac acg ctg tgt ccc gat tct ata 1314			
Leu Met Leu Ala Asn His Leu Val His Thr Leu Cys Pro Asp Ser Ile			
395	400	405	
aca ata gct gag gat gta tca gga atg cca gct ctg tgc tct cca att 1362			
Thr Ile Ala Glu Asp Val Ser Gly Met Pro Ala Leu Cys Ser Pro Ile			
410	415	420	
tcc cag gga ggg ggt ggt ttt gac tat cga cta gcc atg gca att cca 1410			
Ser Gln Gly Gly Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro			
425	430	435	440
gat aag tgg att cag cta ctt aaa gag ttt aaa gat gaa gac tgg aac 1458			
Asp Lys Trp Ile Gln Leu Leu Lys Glu Phe Lys Asp Glu Asp Trp Asn			
445	450	455	
atg ggc gat ata gta tac acg ctc aca aac agg cgc tac ctt gaa aag 1506			
Met Gly Asp Ile Val Tyr Thr Leu Thr Asn Arg Arg Tyr Leu Glu Lys			
460	465	470	
tgc att gct tat gca gag agc cat gat cag gca ttg gtt ggg gat aag 1554			
Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys			
475	480	485	
tcg ctg gca ttt tgg ttg atg gat gcc gaa atg tat aca aac atg agt 1602			
Ser Leu Ala Phe Trp Leu Met Asp Ala Glu Met Tyr Thr Asn Met Ser			
490	495	500	
gtc ctg act cct ttt act cca gtt att gat cgt gga ata cag ctt cat 1650			
Val Leu Thr Pro Phe Thr Pro Val Ile Asp Arg Gly Ile Gln Leu His			

505	510	515	520	
aaa atg att cga ctc att acg cat ggg ctt ggt gga gaa ggc tat ctc 1698				
Lys Met Ile Arg Leu Ile Thr His Gly Leu Gly Gly Glu Gly Tyr Leu				
525	530	535		
aat ttc atg ggt aat gaa ttt ggg cat cct gaa tgg tta gac ttc cca 1746				
Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Leu Asp Phe Pro				
540	545	550		
aga aaa gga aat aat gag agt tac cat tat gcc agg cgg cag ttt cat 1794				
Arg Lys Gly Asn Asn Glu Ser Tyr His Tyr Ala Arg Arg Gln Phe His				
555	560	565		
tta act gac gac gac ctt ctt cgc tac aag ttc cta aat aat ttt gac 1842				
Leu Thr Asp Asp Asp Leu Leu Arg Tyr Lys Phe Leu Asn Asn Phe Asp				
570	575	580		
agg gat atg aat aga ttg gaa gaa aga tat ggt tgg ctt gca gct cca 1890				
Arg Asp Met Asn Arg Leu Glu Glu Arg Tyr Gly Trp Leu Ala Ala Pro				
585	590	595	600	
cag gcc tac gtg agt gaa aaa cat gaa ggc aat aag atc att gct ttt 1938				
Gln Ala Tyr Val Ser Glu Lys His Glu Gly Asn Lys Ile Ile Ala Phe				
605	610	615		
gaa aga gca ggt ctt ctt ttc att ttc aac ttc cat cca agc aag agc 1986				
Glu Arg Ala Gly Leu Leu Phe Ile Phe Asn Phe His Pro Ser Lys Ser				
620	625	630		
tac act gac tac cga gtt gga aca gca ttg cca ggg aaa ttc aaa att 2034				
Tyr Thr Asp Tyr Arg Val Gly Thr Ala Leu Pro Gly Lys Phe Lys Ile				
635	640	645		
gtg cta gat tca gat gca gcg gaa tat gga ggg cat cag aga ctg gac 2082				

Val Leu Asp Ser Asp Ala Ala Glu Tyr Gly Gly His Gln Arg Leu Asp
 650 655 660
 cac agc act gac ttt ttt tct gag gct ttt gaa cat aat ggg cgt ccc 2130
 His Ser Thr Asp Phe Phe Ser Glu Ala Phe Glu His Asn Gly Arg Pro
 665 670 675 680
 tat tct ctt ttg gtg tac att cca agc aga gtg gcc ctc atc ctt cag 2178
 Tyr Ser Leu Leu Val Tyr Ile Pro Ser Arg Val Ala Leu Ile Leu Gln
 685 690 695
 aat gtg gat ctg ccg aat tgaagaggcc tgatttcagc tccaccagat 2226
 Asn Val Asp Leu Pro Asn
 700
 gcagatttgt gttttgttt ctgttatca ctgtcacaca gcttataaca tgtatgcitt 2286
 tcagaataca gtgtcttagc caagccatca agtgtctgaa attcaataatt ggtttatgca 2346
 aatacagcaa acitttatatt aagttagatag gagaataigt ttaaatatt aggaatccia 2406
 gaccatattt tcaagtcatc tttagcagcta ggattctcaa atgaaagtgt tataataat 2466
 atgttaaaaaa catttgctt tcctggctaa ttatttgatc ctttaataat caaatttgaa 2526
 tcatttgtca tgtatgatta ttctgttaa atgtacacag tatttaagat ggatatttg 2586
 tggccttattt tggatgtata tcctttggtc taaattatga ggtaccaaga ttgtttcttt 2646
 gtttctttttt ttcaaaattgt gtttagaaat actgtataaa atatgcagta gtgatataaa 2706
 gaattataatc caaggtataa taaaagccat tacgtatgaa ctcatccgtg tctcatttt 2766
 tggtttattt tggatctct tggccactaa gtatctttt aaatgccagt atctcagtt 2826
 ttctgaagcc ctgaaatggt aattttagca ttccagaaaa tggatgtttcat ttcaatcaat 2886
 aaaaagcttt tgt 2899

<210> 106

<211> 702

<212> PRT

<213> Homo sapiens

<400> 106

Met Ala Ala Pro Met Thr Pro Ala Ala Arg Pro Glu Asp Tyr Glu Ala
1 5 10 15
Ala Leu Asn Ala Ala Leu Ala Asp Val Pro Glu Leu Ala Arg Leu Leu
20 25 30
Glu Ile Asp Pro Tyr Leu Lys Pro Tyr Ala Val Asp Phe Gln Arg Arg
35 40 45
Tyr Lys Gln Phe Ser Gln Ile Leu Lys Asn Ile Gly Glu Asn Glu Gly
50 55 60
Gly Ile Asp Lys Phe Ser Arg Gly Tyr Glu Ser Phe Gly Val His Arg
65 70 75 80
Cys Ala Asp Gly Gly Leu Tyr Ser Lys Glu Trp Ala Pro Gly Ala Glu
85 90 95
Gly Val Phe Leu Thr Gly Asp Phe Asn Gly Trp Asn Pro Phe Ser Tyr
100 105 110
Pro Tyr Lys Lys Leu Asp Tyr Gly Lys Trp Glu Leu Tyr Ile Pro Pro
115 120 125
Lys Gln Asn Lys Ser Val Leu Val Pro His Gly Ser Lys Leu Lys Val
130 135 140
Val Ile Thr Ser Lys Ser Gly Glu Ile Leu Tyr Arg Ile Ser Pro Trp
145 150 155 160
Ala Lys Tyr Val Val Arg Glu Gly Asp Asn Val Asn Tyr Asp Trp Ile
165 170 175
His Trp Asp Pro Glu His Ser Tyr Glu Phe Lys His Ser Arg Pro Lys
180 185 190
Lys Pro Arg Ser Leu Arg Ile Tyr Glu Ser His Val Gly Ile Ser Ser

195 200 205
His Glu Gly Lys Val Ala Ser Tyr Lys His Phe Thr Cys Asn Val Leu
210 215 220
Pro Arg Ile Lys Gly Leu Gly Tyr Asn Cys Ile Gln Leu Met Ala Ile
225 230 235 240
Met Glu His Ala Tyr Tyr Ala Ser Phe Gly Tyr Gln Ile Thr Ser Phe
245 250 255
Phe Ala Ala Ser Ser Arg Tyr Gly Thr Pro Glu Glu Leu Gln Glu Leu
260 265 270
Val Asp Thr Ala His Ser Met Gly Ile Ile Val Leu Leu Asp Val Val
275 280 285
His Ser His Ala Ser Lys Asn Ser Ala Asp Gly Leu Asn Met Phe Asp
290 295 300
Gly Thr Asp Ser Cys Tyr Phe His Ser Gly Pro Arg Gly Thr His Asp
305 310 315 320
Leu Trp Asp Ser Arg Leu Phe Ala Tyr Ser Ser Trp Glu Val Leu Arg
325 330 335
Phe Leu Leu Ser Asn Ile Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp
340 345 350
Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His His His Gly
355 360 365
Val Gly Gln Gly Phe Ser Gly Asp Tyr Ser Glu Tyr Phe Gly Leu Gln
370 375 380
Val Asp Glu Asp Ala Leu Thr Tyr Leu Met Leu Ala Asn His Leu Val
385 390 395 400
His Thr Leu Cys Pro Asp Ser Ile Thr Ile Ala Glu Asp Val Ser Gly

405 410 415
Met Pro Ala Leu Cys Ser Pro Ile Ser Gln Gly Gly Gly Phe Asp
420 425 430
Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile Gln Leu Leu Lys
435 440 445
Glu Phe Lys Asp Glu Asp Trp Asn Met Gly Asp Ile Val Tyr Thr Leu
450 455 460
Thr Asn Arg Arg Tyr Leu Glu Lys Cys Ile Ala Tyr Ala Glu Ser His
465 470 475 480
Asp Gln Ala Leu Val Gly Asp Lys Ser Leu Ala Phe Trp Leu Met Asp
485 490 495
Ala Glu Met Tyr Thr Asn Met Ser Val Leu Thr Pro Phe Thr Pro Val
500 505 510
Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile Arg Leu Ile Thr His
515 520 525
Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly
530 535 540
His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly Asn Asn Glu Ser Tyr
545 550 555 560
His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp Asp Asp Leu Leu Arg
565 570 575
Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met Asn Arg Leu Glu Glu
580 585 590
Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr Val Ser Glu Lys His
595 600 605
Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala Gly Leu Leu Phe Ile
610 615 620

Phe Asn Phe His Pro Ser Lys Ser Tyr Thr Asp Tyr Arg Val Gly Thr
625 630 635 640
Ala Leu Pro Gly Lys Phe Lys Ile Val Leu Asp Ser Asp Ala Ala Glu
645 650 655
Tyr Gly Gly His Gln Arg Leu Asp His Ser Thr Asp Phe Phe Ser Glu
660 665 670
Ala Phe Glu His Asn Gly Arg Pro Tyr Ser Leu Leu Val Tyr Ile Pro
675 680 685
Ser Arg Val Ala Leu Ile Leu Gln Asn Val Asp Leu Pro Asn
690 695 700

<210> 107

<211> 790

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78)..(626)

<400> 107

actgccccaa ggcccccggc gccgcgtccag cgccgcgcag ccaccgcgc cggccggcc 60
tctccttagt cgccgcc atg acg acc gcg tcc acc tcg cag gtg cgc cag 110

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln

1 5 10

aac tac cac cag gac tca gag gcc gcc atc aac cgc cag atc aac ctg 158

Asn Tyr His Gln Asp Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu

15 20 25

gag ctc tac gcc tcc tac gtt tac ctg tcc atg tct tac tac ttt gac 206

Glu Leu Tyr Ala Ser Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp
 30 35 40
 cgc gat gat gtg gct ttg aag aac ttt gcc aaa tac ttt ctt cac caa 254
 Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln
 45 50 55
 tct cat gag gag agg gaa cat gct gag aaa ctg atg aag ctg cag aac 302
 Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn
 60 65 70 75
 caa cga ggt ggc cga atc ttc ctt cag gat atc aag aaa cca gac tgt 350
 Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys
 80 85 90
 gat gac tgg gag agc ggg ctg aat gca atg gag tgt gca tta cat ttg 398
 Asp Asp Trp Glu Ser Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu
 95 100 105
 gaa aaa aat gtg aat cag tca cta ctg gaa ctg cac aaa ctg gcc act 446
 Glu Lys Asn Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr
 110 115 120
 gac aaa aat gac ccc cat ttg tgt gac ttc att gag aca cat tac ctg 494
 Asp Lys Asn Asp Pro His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu
 125 130 135
 aat gag cag gtg aaa gcc atc aaa gaa ttg ggt gac cac gtg acc aac 542
 Asn Glu Gln Val Lys Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn
 140 145 150 155
 ttg cgc aag atg gga gcg ccc gaa tct ggc ttg gcg gaa tat ctc ttt 590
 Leu Arg Lys Met Gly Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe
 160 165 170

gac aag cac acc ctg gga gac agt gat aat gaa agc taaggctcg 636

Asp Lys His Thr Leu Gly Asp Ser Asp Asn Glu Ser

175 180

gctaattcc ccatagccgt ggggtgactt ccctggtcac caaggcagtg catgcatgtl 696

ggggtttcct ttacccccc tataagttgt accaaaacat ccacttagt tcttgattt 756

gtaccattcc ttcaaataaa gaaatttggt accc 790

<210> 108

<211> 183

<212> PRT

<213> Homo sapiens

<400> 108

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln Asn Tyr His Gln Asp

1 5 10 15

Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser

20 25 30

Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp Arg Asp Asp Val Ala

35 40 45

Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln Ser His Glu Glu Arg

50 55 60

Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn Gln Arg Gly Gly Arg

65 70 75 80

Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys Asp Asp Trp Glu Ser

85 90 95

Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu Glu Lys Asn Val Asn

100 105 110

Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn Asp Pro

115 120 125
His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys
130 135 140
Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly
145 150 155 160
Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe Asp Lys His Thr Leu
165 170 175
Gly Asp Ser Asp Asn Glu Ser
180

<210> 109

<211> 3460

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (256)..(1857)

<400> 109

ccctaccgccc cccaaattccg ccctgcggcc gccgcggcg cgctagccgc cactgaggga 60
ccgaccctat aaaggccgct ccgcgagggg tgcgcagcat tcggcagagg gcgcttcgac 120
gggctgggct gtgcgcctgc gcagtgtggg tcgctccga ttccctgccc cggccggccc 180
cgccctggct ccgcaccctc gccccgctct cagccgcgc tctgccccgc agcagccagc 240
cccgtgtccg gcagt atg ttc agc tgg gtc agc aag gat gcc cgc cgc aag 291

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys

1 5 10
aag gag ccg gag ctc ttc cag acg gtg gcc gag ggg ctg cgg cag ctg 339
Lys Glu Pro Glu Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu

15	20	25	
tac gcg cag aag ctg cta ccc ctg gag gag cac tac cgc ttc cac gag 387			
Tyr Ala Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu			
30	35	40	
ttc cac tcg ccc gcr ctg gag gac gct gac ttc gac aac aag cct atg 435			
Phe His Ser Pro Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met			
45	50	55	60
gtg ctc ctc gtg rgg cag tac agc acg ggc aag acc acc ttc atc cga 483			
Val Leu Leu Val Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg			
65	70	75	
cac ctg atc gag cag gac ttc ccg ggg atg cgc atc ggg ccc gag ccc 531			
His Leu Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro			
80	85	90	
acc acc gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc gtg 579			
Thr Thr Asp Ser Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val			
95	100	105	
gtg ccg ggc aac gcg ctc gtg gtg gac ccg cgg cgc ccc ttc cgc aag 627			
Val Pro Gly Asn Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys			
110	115	120	
ctc aac gcg ttt ggc aac gct ttc ctc aac agg ttc atg tgt gcc cag 675			
Leu Asn Ala Phe Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln			
125	130	135	140
ctg ccc aac ccc gtc ctg gac agc atc agc atc atc gac acc ccc ggg 723			
Leu Pro Asn Pro Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly			
145	150	155	
atc ctg tct gga gag aag cag cgg atc agc aga ggc tat gac ttt gca 771			
Ile Leu Ser Gly Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala			

160 165 170
gcc gtc ctg gag tgg ttc gcg gag cgt gtg gac cgc atc atc ctg ctc 819
Ala Val Leu Glu Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu
175 180 185
ttc gac gcc cac aag ctg gac atc tcc gat gag ttc tcg gaa gtg atc 867
Phe Asp Ala His Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile
190 195 200
aag gct ctg aag aac cat gag gac aag atc cgc gtg gtg ctg aac aag 915
Lys Ala Leu Lys Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys
205 210 215 220
gca gac cag atc gag acg cag cag ctg atg cggtt tac ggg gcc ctc 963
Ala Asp Gln Ile Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu
225 230 235
atg tgg tcc ctg ggc aag atc atc aac acc ccc gag gtg gtc agg gtc 1011
Met Trp Ser Leu Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val
240 245 250
tac atc ggc tcc ttc tgg tcc cac ccg ctc ctc atc ccc gac aac cgc 1059
Tyr Ile Gly Ser Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg
255 260 265
aag ctc ttt gag gcc gag gag cag gac ctc ttc aag gac atc cag tca 1107
Lys Leu Phe Glu Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser
270 275 280
ctg ccc cga aac gcc gcc ctc agg aag ctc aat gac ctg atc aag cgg 1155
Leu Pro Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg
285 290 295 300
gca cgg ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa 1203

Ala Arg Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys
 305 310 315
 gag atg ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg 1251
 Glu Met Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Glu Leu Val
 320 325 330
 aac aac ctg gga gag atc tac cag aag att gag cgc gag cac cag atc 1299
 Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile
 335 340 345
 tcc cct ggg gac ttc ccg agc ctc cgc aag atg cag gaa ctc ctg cag 1347
 Ser Pro Gly Asp Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln
 350 355 360
 acc cag gac ttc agc aag ttc cag gcg ctg aag ccc aag ctg ctg gac 1395
 Thr Gln Asp Phe Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp
 365 370 375 380
 acg gtg gat gac atg ctg gcc aac gac atc gcg cgg ctg atg gtg atg 1443
 Thr Val Asp Asp Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met
 385 390 395
 gtg cgg cag gag gag tcc ctg atg cct tcc cag gtg gtc aag ggc ggc 1491
 Val Arg Gln Glu Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly
 400 405 410
 gcc ttt gac ggc acc atg aac ggg ccg ttc ggg cac ggc tac ggc gag 1539
 Ala Phe Asp Gly Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu
 415 420 425
 ggg gcc ggc gag ggc atc cac gac gtg gag tgg gtg gtg ggc aag gac 1587
 Gly Ala Gly Glu Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp
 430 435 440
 aag ccc acc tac gac gag atc ttc tac acg ctg tcc cct gtc aac ggc 1635

Lys Pro Thr Tyr Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly
 445 450 455 460
 aag atc acg ggc gcc aac gcc aag aag gag atg gtg aag tcc aag ctc 1683
 Lys Ile Thr Gly Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu
 465 470 475
 ccc aac acc gtg cta ggg aag atc tgg aag ctg gcc gac gtg gac aag 1731
 Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys
 480 485 490
 gac ggg ctg ctg gac gac gag gag ttc gcg ctg gcc aac cac ctc atc 1779
 Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile
 495 500 505
 aag gtc aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac 1827
 Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His
 510 515 520
 ctg gtg ccg ccc tcc aag cgc aga cat gag tcatggcgcc cggccccgca 1877
 Leu Val Pro Pro Ser Lys Arg Arg His Glu
 525 530
 cctgccattt gcacgcccgg ccgggaggca gagacggggg gaggggaagc ctcaccattt 1937
 ctcaagggtcc ataaagactg agcggatgtt tcctcgcctc tcgaaaagga aaaccaccat 1997
 cttctttta aggctgttcc tgggcctggc gggggaggca ggggtgagag gatggaattt 2057
 tgcacaag aactgtggct atttaatat ataacgttag aggctgcgtt ctgtcgcc 2117
 gcctccccctg tgtgccagcc ctgtgtgcac ggcctctgcc ccccgccctt gtgtgtggc 2177
 tggagctgga cagtgcagtg actgcgaccg tgggggagcc aggtcgccct ttggcagct 2237
 gctaggctgaa ggctgcattt acaggaacac caggcacccctt ccgtgtgcctt ctgagctgag 2297
 gtgtgttacac gggaccgtgg ctcccttccctt cacctggctc tgcctccccctt gtgtgtggc 2357
 gcgaaatgggg tttttgtgcc ttccccctccc gggcccgagcc tccccgtgcg cggccctgc 2417

cctttccccc cgcgccccac cggctccgac gcgcaccccc gctcagcagt cacagaagca 2477
 gggcccgagcc accttggct tttttggga gttcagggga gtaggagaat gtcttccaga 2537
 aaaatacata agctagttc tttttgtaa agtgataatct ttcatatgtt accaaaggcc 2597
 ccaataacit cccaaacctt gttcaaaagc tttttttt gtctccctt cccaccctcc 2657
 agccaaggag cagccctgcc cagggaaatt tagtgtggg tacccgggg aaccccggtt 2717
 cctggacccc agtggatgtt ttcctggctg aggaagggtg gtcatccag ctccctgcct 2777
 accctctcac ttaactggag ctttggacg caccctccac agtgggaggt ggtggtgccc 2837
 tggcggtggc gggccctcac gacagcttgg tgctggtaag aggaagcccg tggttctggc 2897
 taggcctctca tgcctcagaca gccccggacca gggaaaacc cagcccttc tgcataatcccc 2957
 cttcatttcc taccttcctt ctcctctgt ttagcaaagg agggcagctc acttggatgt 3017
 ctttacaacg cccctggccc caggttggac aataagaaac cagaaccttgc cggccctgt 3077
 gccccggcca gttcaggccg ctcctccctc ctctgcctgg ggccatttag cccctccctc 3137
 cagggggcccg ggtgcgttgc caagccagtg gccactgtcc gggctgtat ggcaccaagg 3197
 caggaggagc accaggttacc acacagctgg gtttccacc aggtttccc gcgaaaaatct 3257
 cagggagctt ctccccagcg ctgcgtggag tctgcaggaa ctggcttgt ttccttagc 3317
 ccgtcactcc atacagtatt aggtgaggat ggtgcgggc gttgtcccttgc cggaaatgc 3377
 actgttgaag ttgcagtggc ttgttccacac ctgtggaaag agaagtgaag actttctct 3437
 tgcattaaaa agtctgaact gtg 3460

<210> 110

<211> 534

<212> PRT

<213> Homo sapiens

<400> 110

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys Lys Glu Pro Glu

1

5

10

15

Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu Tyr Ala Gln Lys

20 25 30

Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu Phe His Ser Pro

35 40 45

Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu Leu Val

50 55 60

Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu Ile Glu

65 70 75 80

Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr Asp Ser

85 90 95

Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro Gly Asn

100 105 110

Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn Ala Phe

115 120 125

Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Pro

130 135 140

Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly

145 150 155 160

Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala Ala Val Leu Glu

165 170 175

Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu Phe Asp Ala His

180 185 190

Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile Lys Ala Leu Lys

195 200 205

Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Gln Ile

210 215 220

Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ser Leu

225 230 235 240

Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser
245 250 255
Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu
260 265 270
Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn
275 280 285
Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala
290 295 300
Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn
305 310 315 320
Val Phe Gly Lys Glu Ser Lys Lys Glu Leu Val Asn Asn Leu Gly
325 330 335
Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp
340 345 350
Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe
355 360 365
Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp
370 375 380
Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu
385 390 395 400
Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly
405 410 415
Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu
420 425 430
Gly Ile His Asp Val Glu Trp Val Val Lys Asp Lys Pro Thr Tyr
435 440 445

Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly

450 455 460

Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val

465 470 475 480

Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys Asp Gly Leu Leu

485 490 495

Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile Lys Val Lys Leu

500 505 510

Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val Pro Pro

515 520 525

Ser Lys Arg Arg His Glu

530

<210> 111

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)..(724)

<400> 111

ggtcgggtgtc ctgtgaccc tgcctttgtc tggctgtcac cggtggact ggcggggact 60

gtgtgattaa cctccatitc agctaatac atg gga gag att aaa gtc tct cct 112

Met Gly Glu Ile Lys Val Ser Pro

1 5

gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg 160

Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val

10	15	20	
gat gat gat gac agt aag ata tgg tcg ctc tat gac gcg ggc ccc cga			208
Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg			
25	30	35	40
agt atc agg tgt cct ctc ata ttc ctg ccc cct gtc agt gga act gca			256
Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala			
45	50	55	
gat gtc ttt ttc cgg cag att ttg gct ctg act gga tgg ggt tac cgg			304
Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg			
60	65	70	
gtt atc gct ttg cag tat cca gtt tat tgg gac cat ctc gag ttc tgt			352
Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys			
75	80	85	
gat gga ttc aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat			400
Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His			
90	95	100	
ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa			448
Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu			
105	110	115	120
tac act cac aaa tct cct aga gtc cat tcc cta atc ctc tgc aat tcc			496
Tyr Thr His Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser			
125	130	135	
ttc agt gac acc tct atc ttc aac caa act tgg act gca aac agc ttt			544
Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe			
140	145	150	
tgg ctg atg cct gca ttt atg ctc aaa aaa ata gtt ctt gga aat ttt			592
Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe			

155 160 165
tca tct ggc ccg gtg gac cct atg atg gct gat gcc att gat ttc atg 640
Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met
170 175 180
gta gac agg cta gaa agt ttg ggt cag agt gaa ctg gct tca aga ctt 688
Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu
185 190 195 200
acc ttg aaa ttg tca aaa ttc tta tgt gga acc tca taaaattcgg 734
Thr Leu Lys Leu Ser Lys Phe Leu Cys Gly Thr Ser
205 210
ggacataacct gtaacttatta tggatgtgtt tgatcagagt gcgccttcaa ctgaagctaa 794
agaagaaaatg tacaagctgt atccctaattg cccccaaagag gctcatctga aaacaggagg 854
caatttccca tacctgtgca gaagtgcaga ggtcaatctt tatgtacaga tacatttgc 914
kgcaattccw kggrggaccm aatacgccgc ctttgaccca tcaatggtca gtggccgagga 974
gcttgagggtg cagaaaggca gccttggcat cagccaggag gagcagtagt gtgtctctcg 1034
ctgtcaatga tgagttgacc cggtgtgttc ttgtatagtc agtgggcattc agcacccgtt 1094
cagccggcct tttcccttcag gttcgtcagg ctcaccgggtt ctcaactgtgtt ctggaaagta 1154
ggactgtatgg tcatcttcat gacaggccgc atctccacta agcctgtgta actgtttccct 1214
ctttggtttt cttagctttt gaatttgaag aagtactttt gaagactccc attttaagaa 1274
ccgtgcaaattt tttgctacca aaagtcttca ccactgtgtt cttaagtgaa tgttaatttc 1334
tgaggtttgg gactttgtgg tggttttttt cttcttttct tttccatttct tcttttttc 1394
ttttatgtt gtttgctgtt aatgctgcac atccagatttgc catacagga cattggttat 1454
tttatgtttt cttggatata accatgtatca gagtgccatg gccactaccc cactgtttgc 1514
tctcctgcaa atcaactgtt tttatattac actttaaacaa attgttttga gtgttagcta 1574
ctgcctttctt agatatttagt catttggaat aaaaattcaa tttcacttg 1622

<211> 212

<212> PRT

<213> Homo sapiens

<400> 112

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr

1 5 10 15

Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Asp Ser Lys Ile Trp

20 25 30

Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe

35 40 45

Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu

50 55 60

Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val

65 70 75 80

Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp

85 90 95

His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly

100 105 110

Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val

115 120 125

His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn

130 135 140

Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu

145 150 155 160

Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met

165 170 175

Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly

180

185

190

Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Lys Leu Ser Lys Phe Leu

195

200

205

Cys Gly Thr Ser

210

<210> 113

<211> 2391

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (360)

<220>

<221> unsure

<222> (49)

<223> g or t

<220>

<221> unsure

<222> (51)

<223> a or t

<220>

<221> unsure

<222> (54)

<223> t or c

<220>

<221> unsure

<222> (55)

<223> g or t

<220>

<221> unsure

<222> (56)

<223> g or t

<220>

<221> unsure

<222> (91)

<223> g or c

<220>

<221> unsure

<222> (101)

<223> t or c

<220>

<221> unsure

<222> (103)

<223> g or t

<220>

<221> unsure

<222> (325)

<223> t or c

<220>

<221> unsure

<222> (425)

<223> g or t

<220>

<221> unsure

<222> (688)

<223> g or c

<220>

<221> unsure

<222> (1459)

<223> g or t

<220>

<221> unsure

<222> (1705)

<223> g or t

<400> 113

gac ccg ttc cat gca gtt gta tac ata gtg ttc atg ctg ggc tcc tgt 48

Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

1

5

10

15

kcw tty kkc tcc aaa acg tgg att gag gtc tca ggt tcc tct scc aaa 96

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

gat gyt kca aag cag ctg aag gag cag cag atg gtg atg aga ggc cac 144

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35

40

45

cga gag acc tcc atg gtc cat gaa ctc aac cgg tac atc ccc aca gcc 192

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50

55

60

gcg gcc ttt ggt ggg ctg tgc atc ggg gcc ctc tcg gtc ctg gct gac 240

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp
65 70 75 80
ttc cta ggc gcc att ggg tct gga acc ggg atc ctg ctc gca gtc aca 288
Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr
85 90 95
atc atc tac cag tac ttt gag atc ttc gtt aag gag yaa agc gag gtt 336
Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val
100 105 110
ggc agc atg ggg gcc ctc ttc tgagcccgtc tccggacag gttgaggaag 390
Gly Ser Met Gly Ala Leu Leu Phe
115 120
ctgctccaga agcgcctcgg aaggggagct ctcakcatgg cgctgtgc tgcggcalat 450
ggacttttaa taatgtgtt tgaatttcgt attctttcat tccactgtgt aaagtgttag 510
acatittcca atttaaaatt ttgcctttta tcctggcac tggcaaaaaga actgtgaaag 570
tgaatttta ttcagccgac tgccagagaa gtggaaatgg tataggatg tccccaaatg 630
tccatgtaac ttttgtttta acccttgcac cttctcagtg ctgtatgcgg ctgcagcstc 690
ctcacctgtt tccccacaaa gggaaatttc cactctgtt ggaagcacaa acacctggaa 750
atgtctacgt ttcattttgg caagtarggt gtgaagcctg ggagcagatc atgtatttcc 810
cgagagacgtg ggaccttgct ggcgtgtc cttcacaatc aggctggaa atatctggct 870
taggactgtt tctctctaag acaccattgt ttcccttat tttaaaatgt attttttaa 930
ggacagaact tcttccaaaa gagagggatg gcttccag aagacactcc tggccatctg 990
tggatttgtc tgtgcaccta ttggcttcc tagctgactc ttctgggtgg gcttagatgc 1050
tgcctgtttc tgctagctcc gtgtttagtc cacttgggtc atcagctctg ccaagctgag 1110
ccctggccaaag cttagtggac agacccttgc agtgtatgtcc gtttgcctcag attctggccag 1170
tcatcactgg acacgtctcc tcggcagctg cccttagcaag gggagacatt gggtagct 1230
tcagacatgg acagaaactg acttagtgct cacaagcccc tacaccttgc tggctgaag 1290
atcacccagc tggttcaga attttcttac tggctttagg actgcacgca agtraghcaga 1350

caccaccgac ttcccttctg cgtcaccagt glcgltcagca gagagaggac agcacaggct 1410
caaggtttgtt agtgaagtca gtttcgggt gcatggcclg tggtggtgkt gatcagtgc 1470
tccagtggtt gaaataagaa gactcatgtt tatgtctgga ataagttctg tttgtgctga 1530
caggltggcct aggtccctgga galgagcacc ctctctctgg cctttaggga gtcccctctt 1590
aggacaggca ctgcccagca gcaagggcag cagagltggg tgctaagatc ctgaggagct 1650
cgaggtttcg agctggcttt agacatttgtt gggaccaagg atgttttgcg ggatkccctg 1710
atcclaagaa gggggccctgg gggtgcgicg agcctgtcgg ggagacccca ctctgacagt 1770
gggcacacgg cagccctgcaa agcacaggc caccgcccaca gcccgccaga ggggcacact 1830
ctggagacct tgctggcagt gctagccagg aaacagagtg accaagggac aagaagggac 1890
ttgcctaaag ccaccctagca actcagcagc agaaccctaga tgggccccag gcicctccat 1950
atggcccagg gcttaccacc ctatcacacg tggccttgcgtt cctagaccca glcctgagca 2010
ggggagaggc tcitgagacc ttagtgccttc ctacccacat ggttctccca ctgcccgtc 2070
tgctctgctg ctacagaggg gcagggccctc ccccagccca cgcttaggaa tgcttggcct 2130
ctggcaggca ggcagctgta cccaaagctgg tggcaggggg gctggaaaggc accaggccctc 2190
aggaggagcc ccatagtcctc gcctgcagcc tggtaaccatc ggctggccc tgcaaggccc 2250
acactcacgc cctgtgggtg atggtcacgg tgggtgggtg gggctgacc ccagcttcca 2310
ggggactgtc actgtggacg ccaaaatggc ataactgaga taaggtgaat aagtgacaaa 2370
taaagccagt tttttacaag g 2391

<210> 114

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (17)

<223> unknown

<220>

<221> unsure

<222> (18)

<223> unknown

<220>

<221> unsure

<222> (19)

<223> unknown

<220>

<221> unsure

<222> (31)

<223> unknown

<220>

<221> unsure

<222> (109)

<223> unknown

<400> 114

Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

1

5

10

15

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35

40

45

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50

55

60

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp

65 70 75 80
Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr
85 90 95
Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val
100 105 110
Gly Ser Met Gly Ala Leu Leu Phe
115 120

<210> 115

<211> 599

<212> DNA

<213> Homo sapiens

<400> 115

gggtatggaa ttggctgagg atcaaacgt a ttaggtgaa aggataccag gatgttgcta 60
aaggtagggg acagtttggg ttgggactt accggggiga ttttagatct ggaaccccca 120
agtgaggctg gagggagttt aggtcagttt ggaagatagg gtggcacag ggtgtttgg 180
aatgaaaagag tgaccctaga gggctccctt ggcctcagga atgccttcgc tgctgtgaag 240
atgagaaggt gctcttactc agttaatgtat gatgtactat atttacaaa gcccctacct 300
gctgctgggt ccctttagc acaggagact tgggctaagg gcccctccca ggaaaggac 360
accatcaggc ctctggctga ggcagtagca tagaggatcc atttctacct gcatttccca 420
gaggactagc aggaggcage cttgagaaac cggcagttcc caaagccagc gcctggcgtl 480
tctctcattt tcaactgcctt ctcccccaacc tctcccttaa cccactagag attgcctgtg 540
tctgcctct tgcctcttgt agaatgcagc tctggccctc aataaatgct tcctgcatt 599

<210> 116

<211> 364

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (134)

<223> a, c, g or t

<220>

<221> unsure

<222> (135)

<223> a, c, g or t

<220>

<221> unsure

<222> (179)

<223> g or a

<400> 116

tgcgtatcaca tagttctca tccccaccga agtgcattaa atggcagtag aaatcactat 60

acagtgccttc caggggcgca ttgggggaa tgagaatgt gatgaagtagt aaatgtctgc 120

cacagttcca ggannggta ggttagcagtg tgtgtgttat gtgccactga ccctgaaara 180

tgtgccatag cccaaaggccaa ttgaaattga tcagggggcc aggcattgtg gctcatgcct 240

gtaatcccag caccttggga agctgaggtg ggaggattgc ttgaaaccag gagttcaaga 300

ccagcctgtg caacatagca aaacccatc tctacaaga taaaaataa aaaattagct 360

gggc 364

<210> 117

<211> 852

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(217)

<220>

<221> unsure

<222> (37)

<223> a, c, g or t

<400> 117

gttcagtttc aagtttacaa gaggc atg gat gga gtn gtg acg ttc ttg aca 52

Met Asp Gly Xaa Val Thr Phe Leu Thr

1 5

agc tgg gct aac ctt tcc cga act tgt ttc ccg gag gca agg tgc tcg 100

Ser Trp Ala Asn Leu Ser Arg Thr Cys Phe Pro Glu Ala Arg Cys Ser

10 15 20 25

gtg acc cag cgc atc tta acc ttg ggt ctc cta ggc tcg agg cta ggg 148

Val Thr Gln Arg Ile Leu Thr Leu Gly Leu Leu Gly Ser Arg Leu Gly

30 35 40

cat tac gtt tcg tgg aac caa agc agc caa ttg cat agc aag tat ttt 196

His Tyr Val Ser Trp Asn Gln Ser Ser Gln Leu His Ser Lys Tyr Phe

45 50 55

cct gca ttc caa tta aat gct taagaaaaag cagcatccta taaaattgtg 247

Pro Ala Phe Gln Leu Asn Ala

60

atcataaaaca tccatttccc tcagcttttg tgagtgcctt gacttacagc caacatcaact 307
 gittaactca gictgtttaa aaacaaactt ttctggtggt tgataacaga gagttgciccc 367
 ctgagccatc agggtcctgg gagctggaag tgaaagggtt attaacatcc tacclttatg 427
 cagctgttgg ctgaccagaa taaactccct gcigagltca agctttaaat ggaatggatg 487
 caaatgatgt tgtttccatt agagcaggtg ctcacagcat tctgattggc ctgagcagac 547
 cgaggctatg gctgttggca caagcttagc atccctggaca tcttgtcaaa gaacctcaact 607
 cacccctctg gcctctacag ccctcagagg agagaaaacc aattctccaa caaacaggtc 667
 tctccaaatat ggtggcgctg gcaggcttag gtttagaaaa tcctgactgt taaaggcggt 727
 tgaatacatc acattcctat gcaaataatgttt ttaatctcca gtttaatgtt gtttatttt 787
 cctatatgtt aagtatittt atacggcttg tatcatgata gtttagcaat aaaacagttg 847
 gaagc 852

<210> 118

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (4)

<223> unknown

<400> 118

Met Asp Gly Xaa Val Thr Phe Leu Thr Ser Trp Ala Asn Leu Ser Arg

1

5

10

15

Thr Cys Phe Pro Glu Ala Arg Cys Ser Val Thr Gln Arg Ile Leu Thr

20

25

30

Leu Gly Leu Leu Gly Ser Arg Leu Gly His Tyr Val Ser Trp Asn Gln

35

40

45

Ser Ser Gln Leu His Ser Lys Tyr Phe Pro Ala Phe Gln Leu Asn Ala

50

55

60

<210> 119

<211> 1156

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (524)..(1105)

<220>

<221> unsure

<222> (10)

<223> a or t

<400> 119

cggcaactgw gaggaagcaa agggaaaaaa actccattaa aaagcccagc ttccctccat 60
gttagatgtg acttggaaaa tgagaaagat ttagcaaaat tccaccgtat ctttgccag 120
gctagagaca gggagagcag agtaaaaccc tcaggctgct gaaatttcta ggctgttagg 180
aagccccctcg aattctgtga aaatgagggt ttcttaactc acactgagag cggaaagggg 240
cagacccttt tcataactcc ctcaagtgtg tggcacccctt ctttaccagc atggtaagca 300
acaggacata tcccagcctc ggacatgtct gtatgtcca aggtacccaa agtcagacag 360
agtaaaactca agcctggcac tggcttctg ccgcattcatg tgcttggaa aaagcaggag 420
aagcaatagc agcaggagtc cccagcagct ggagccgcaa gaatgaactg caaagaggga 480
actgacagca gctgcggctg cagggggcaa cgacgagaag aag atg ttg aag tgt 535

Met Leu Lys Cys

1

gtg	gtg	gtg	ggg	gac	ggt	gcc	gtg	ggg	aaa	acc	tgc	ctg	ctg	atg	agc	583
Val	Val	Val	Gly	Asp	Gly	Ala	Val	Gly	Lys	Thr	Cys	Leu	Leu	Met	Ser	
5																
	10															20
tac	gcc	aac	gac	gcc	tcc	cca	gag	gaa	tac	gtg	ccc	act	gtg	ttt	gac	631
Tyr	Ala	Asn	Asp	Ala	Phe	Pro	Glu	Glu	Tyr	Val	Pro	Thr	Val	Phe	Asp	
25																35
cac	tat	gca	gtt	act	gtg	act	gtg	gga	ggc	aag	caa	cac	ttg	ctc	gga	679
His	Tyr	Ala	Val	Thr	Val	Thr	Val	Gly	Gly	Lys	Gln	His	Leu	Leu	Gly	
40																50
ctg	tat	gac	acc	gcg	gga	cag	gag	gac	tac	aac	cag	ctg	agg	cca	ctc	727
Leu	Tyr	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asn	Gln	Leu	Arg	Pro	Leu	
55																65
tcc	tac	ccc	aac	acg	gat	gtg	ttt	ttg	atc	tgc	tcc	tct	gtc	gta	aac	775
Ser	Tyr	Pro	Asn	Thr	Asp	Val	Phe	Leu	Ile	Cys	Phe	Ser	Val	Val	Asn	
70																80
cct	gcc	tct	tac	cac	aat	gtc	cag	gag	gaa	tgg	gtc	ccc	gag	ctc	aag	823
Pro	Ala	Ser	Tyr	His	Asn	Val	Gln	Glu	Glu	Trp	Val	Pro	Glu	Leu	Lys	
85				90												100
gac	tgc	atg	cct	cac	gtg	cct	tat	gtc	ctc	ata	ggg	acc	cag	att	gat	871
Asp	Cys	Met	Pro	His	Val	Pro	Tyr	Val	Leu	Ile	Gly	Thr	Gln	Ile	Asp	
105																115
ctc	cgt	gat	gac	cca	aaa	acc	ttg	gcc	cgt	ttg	ctg	tat	atg	aaa	gag	919
Leu	Arg	Asp	Asp	Pro	Lys	Thr	Leu	Ala	Arg	Leu	Leu	Tyr	Met	Lys	Glu	
120																130
aaa	cct	ctc	act	tac	gag	cat	ggt	gtg	aag	ctc	gca	aaa	gcg	atc	gga	967
Lys	Pro	Leu	Thr	Tyr	Glu	His	Gly	Val	Lys	Leu	Ala	Lys	Ala	Ile	Gly	

135 140 145
gca cag tgc tac ttg gaa tgt tca gct ctg act cag aaa ggt ctc aaa 1015
Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys
150 155 160
gcg gtt ttt gat gaa gca atc ctc acc att ttc cac ccc aag aaa aag 1063
Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His Pro Lys Lys
165 170 175 180
aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca att atc 1105
Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser Ile Ile
185 190
tgagggttgtc tgggacactgc ctccacccca tccagggatg agaatggcag c 1156

<210> 120

<211> 194

<212> PRT

<213> Homo sapiens

<400> 120

Met Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys
1 5 10 15
Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro
20 25 30
Thr Val Phe Asp His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln
35 40 45
His Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln
50 55 60
Leu Arg Pro Leu Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe
65 70 75 80

Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val
85 90 95
Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly
100 105 110
Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu
115 120 125
Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala
130 135 140
Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln
145 150 155 160
Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His
165 170 175
Pro Lys Lys Lys Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser
180 185 190
Ile Ile

<210> 121

<211> 1732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (259)

<220>

<221> unsure

<222> (28)

<223> a, c, g or t

<220>

<221> unsure

<222> (388)

<223> g or a

<220>

<221> unsure

<222> (631)

<223> a or t

<220>

<221> unsure

<222> (637)

<223> g or a

<220>

<221> unsure

<222> (638)

<223> g or a

<220>

<221> unsure

<222> (639)

<223> g or a

<400> 121

g gac att gag tcc aag gag cag gtg cgn acc ctc acg ggc cac gtg ggc 49

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

acc gtg tat gcc ctg gcg gtc atc tcg acg cca gac cag acc aaa gtc 97

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20 25 30
ttc agt gca tcc tac gac cgg tcc ctc agg gtc tgg agt atg gac aac 145
Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn
35 40 45
atg atc tgc acg cag acc ctg ctg cgt cac cag ggc agt gtc acc gcg 193
Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala
50 55 60
ctg gct gtg tcc cgg ggc cga ctc ttc tca ggg gct gtg gat agc act 241
Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr
65 70 75 80
gtg aag gtt tgg act tgc taacaggatc caggccaggc tgtggtttcc 289
Val Lys Val Trp Thr Cys
85
cctgaaccag ccctggacct ttctgagcca ggctggccac atgggggtt ctggggttt 349
ctgcctgccc cgtggcata ggtggacagg ctctggcarg cggcagtgc cctccccgtc 409
ccatgctcgg cgagccccc tctactcggc actgtcccttg ctgcccagcc cctctctggg 469
tgccaggtac gacgcttgcc cggcccccacc ctccatcccc accctccatc cccaccctag 529
atggagcgag ggcctttta ctacacctttt ctaccgtttt tagactgtat gtagatttgg 589
ttacctcctg gttgaaataa atgctccaca gactgtgaaa awaaaaarrr acaamtcctc 649
gggacaaggg ggctgtgtgt ggccttgagg ttggtgtgca caggcactgg ctgtgtgag 709
tggggggca tggggcagtt tccttggtg gacccagga ctctggccca ctccggggct 769
ccccctccctg ctaggaggca acicgtcaca cccaaagctgc tggcctccag tcccatctcc 829
cccaacacat gtgcccccaa aaagtgagcc aggcacccctt gtttctgtctt gtttattgac 889
agccgacgga ggccttgcc cagacccccc ctgcccaccc gctggagccc agcctgtgcc 949
gcctctgag gagaggcctg gggggacagc tggcacgtc cactcgcagg gaaacacggg 1009
gtgagacagc aggaagggc cctgcacgccc gggacgccc acctccaccc cgcctccacc 1069
cgccccacac cacaatcgct ggtttgcgc atttttaaa tttttttt aagaaaacgtc 1129

aaagtgtgc ccaacactgt gatatcagcaa acacgataga ggagaccagt cagtaacttct 1189
 tggagggggc aggaggagag aggaaaaggg agggcgagaa tgaccacaca acacagcctt 1249
 ggaccatgag cagaagcgic cgtggaaact ccactgggtt ggtatggctg cctgcacagc 1309
 cccggagag gggccaggc acacccttag agggagctgc aagcccgigg cctggctgc 1369
 tacatgcctt gttccacgt ggctgccacg ctgacacacc cacattcacc aaacccaccc 1429
 gcgcctggg acgcagccac gccaggagga ggacacggcc gccgagagca aggcacaacc 1489
 tcgatctt gggcgaga gaacttagga gagaagcacg gaggagcccc cggcagagca 1549
 cccgcggccgg ggcccccagcc ttccacctgt gctagcagcc tggggctcc actctggccg 1609
 gaggaaggac cgccaggaga cagcctggc ctctaacagc ttttgtccgg agctagactt 1669
 cgtgtccctt cagttggtaa atggttttct atagaatcaa taatatttct ttctttaaat 1729
 ata 1732

<210> 122

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (9)

<223> unknown

<400> 122

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1	5	10	15
---	---	----	----

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20	25	30
----	----	----

Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn

35	40	45
----	----	----

Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala
50 55 60
Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr
65 70 75 80
Val Lys Val Trp Thr Cys
85

<210> 123

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (168)..(350)

<220>

<221> unsure

<222> (343)

<223> g or a

<220>

<221> unsure

<222> (422)

<223> t or c

<220>

<221> unsure

<222> (457)

<223> g or c

<400> 123

gttctttccc ccacccgtgcc acaccctggg agaaaaaaact agacttggc ttcagaaagc 60
 acagatgtga cccaggctt ctaaagagac aactccacag ccctgtggAAC acactcttga 120
 gccaaacttg gttgaagact aggtcttccc tggcaagttc cggaaga atg gac tta 176

Met Asp Leu

1

ctg act ttt atc aac tct tct cac tgc caa ggc caa cag cat ctg agg 224

Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gln Gln His Leu Arg

5 10 15

tat agc ttt ttg gga gta cct gct ttc ttg cct cct gga gga tat ttt 272

Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly Gly Tyr Phe

20 25 30 35

ctg tcc tgg ggc ttc atg gcc cct ctc ttc cct gtt aca cat tgc tgt 320

Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr His Cys Cys

40 45 50

gct tca gag cct ttg cag ctg cra cct agt tgaatccaca taggsttcct 370

Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

55 60

tccacacgggt gggaggatc ttgttgttt cactcacagg accagggagt tyttcaatca 430

ggagggtgggt ttttgttccc ttcaaggscct tggcaacatc tagagacagt ttgtattgcc 490

acgcctggag tggatgtgt gtgtactgg catctagtgg ctgciaaaca tcctacactg 550

cataggatag tccccactac ccccgccaa gaattatctg actccagggg tca 603

<210> 124

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (59)

<223> unknown

<400> 124

Met Asp Leu Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln

1

5

10

15

His Leu Arg Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly

20

25

30

Gly Tyr Phe Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr

35

40

45

His Cys Cys Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

50

55

60

<210> 125

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (775)..(1017)

<220>

<221> unsure

<222> (200)

<223> g or a

<400> 125

tatgcgagcc aatattgaga gaggaatttt gctgagggtt tctctgaggt ttttttgatg 60

ctttagatgg aactatttt taaaaaaagc cattccccac ccaaggacac agtggatgtg 120

tttccctga ctccagcagg gcaaggaatg taaccgagag gtgtgtggg ctgggctctg 180
 gtgcctctt ccctggcccr gaacacctct cctcctgatt cccttggcac ctgtcttc 240
 tgcgtgttta cctgtctccc tgcctgccca tctgcacatt ttgcagccca ctctgacttc 300
 catctggggg ctgagaccac ccttgcctgc ccccttcattt ctgccttaag aatgtccctt 360
 taggctggc atggtgtca cgcctgtaaac cccagcactt tgggaggcgg agacggcag 420
 ataacctgag gtcaggattt cgagaccaac ctgacctaca tggagaaaact ccgcctctag 480
 taaaaataca aaatttagccg ggcacatggtgg tgcacgcctc taatcccagc tactcgagg 540
 gctgaggcag gagaatcaact tgaacccggg aagtggaggt tgcatgtgagc caagagtaca 600
 ccactgcact ccagcctggg caacagagcg agactccgtc taaaaaaaaa aaaaaaaaaaag 660
 aacgccttt tactgtcctc atcatcccag tttgaggcag tgctggagtg gggaggccg 720
 tcttagacca tagaggttgg aagacgctga gagatcatcc agcccagccc ctgt atg 777

Met

I

tta cag agc aga aga cag atg ccc aaa cag gag aag gca ctt gcc cac 825
 Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala His

5

10

15

ggt cat acg gca ggt tgc cac aaa acc aag atg gca gcc ctt cct cag 873
 Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro Gln

20

25

30

cgt gcc tca ctg cca ctc cca gag cca ggg agc ccc ata aaa ccc aca 921
 Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro Thr

35

40

45

tca tgl ctt aag agt ata tct ggc tcc ttg acc agc aat cgg ccc tgg 969
 Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro Trp

50

55

60

65

gag cca cca ggt ggg aaa agc gcc tct gcc aga gtc cag gcc ttg gga 1017

Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly

70

75

80

tgacagacag ctggccgca cactcgggcc ccactcaagg atgttagggcc ttttctggcc 1077
 cctgaccctt ccctggcat tgggagcggtg gggacggggc tggccttggg aggagcggca 1137
 gggcatacac ctccctctgc tgcttcctcc tgctccatcc ctaaggccc tggggctgc 1197
 ccagctgcct ctatgcctt ctggggctc cagccactg ctgacacttc tgcaatccag 1257
 agaaaacacta aataaagcaa tacgtgtttg cc 1289

<210> 126

<211> 81

<212> PRT

<213> Homo sapiens

<400> 126

Met Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala

1

5

10

15

His Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro

20

25

30

Gln Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro

35

40

45

Thr Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro

50

55

60

Trp Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu

65

70

75

80

Gly

<210> 127

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (734)..(886)

<220>

<221> unsure

<222> (276)

<223> g or t

<400> 127

tttttagaca gagttttgct ctcatggcc aggctggagt gcgggttgtc tatttcagct 60
 caccacaacc tctgcctcct gggttcaagg gatttccttg ctttagcctc ccgaatagct 120
 ggaattacag gcacgcacca ccatgcctga ctaattttgt atttttagta gacatgggt 180
 ttctccatgt tggtcaggct ggtctcaaac tcccacccctc aggtgatccg cccaccccg 240
 cctccctgagg tggctgagat tacaggcgtg caactkgtgc cagcttgcta attttcacag 300
 aagttgatgg caattttca catgtaaaca gtgccagtgc acagaacctt tatatatttt 360
 ttgaagccag tactgtc tcataataac aaagctgctt caaggatgag accttttct 420
 aaaagcatgt aatgtgagaa gccggcctgc cttatttct tttttttttt ttaatgatta 480
 aaaatagttt gtggcaaggc acgggtggctc aggcctgtaa ttctagcact ttgggaggcc 540
 gaggcaggag gattactga gcctacaagt ttgatggcc agcatgcaca gcatagcaag 600
 actgcatactc tacagagagt aaaaaaaatt acccgaglgt ggtgatgtgc atctgtaaatc 660
 tcagctactt gggaggctga ggtgagagga tcacttgagc ttgggtgagg tgaggctgca 720
 gtgagtcctg atc atg ctg ctg cac tca atc ttg gac aac aga gca aga 769

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg

1

5

10

ccc tgt ctc aaa aaa aaa aat ata tat ata tat ata tat tat ttt 817

Pro Cys Leu Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe
 15 20 25
 tat gag gtg aag tgc atc aaa ctt ggg aaa gat ttg agg agg ctg gga 865
 Tyr Glu Val Lys Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly
 30 35 40
 acc tcc tgg aaa acc act cct tgaagaaaga tatgagagac atttagaagt 916
 Thr Ser Trp Lys Thr Thr Pro
 45 50
 gat tcc tgc ttcagaagga ggtggattca aatacatcaa aagtcccttc ctctgctaag 976
 tgg tttatagt tcaatgaata atttcaatat ttgtatgtgt tctgtcatt ttatttttt 1036
 ctgaaaaact tccaaaatt tgaaaataaa attacagcct ttttttctt 1085

<210> 128

<211> 51

<212> PRT

<213> Homo sapiens

<400> 128

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg Pro Cys Leu Lys

1 5 10 15

Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe Tyr Glu Val Lys

20 25 30

Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly Thr Ser Trp Lys

35 40 45

Thr Thr Pro

50

<210> 129

<211> 1544

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1076)

<223> g or a

<400> 129

gctttgaact tactcaggaa agccagcccc cataatattt tattacaaa cagttatcgct 60

ttgttaggaa ggatctggaa taatcttcaa gggaaatgcag agtttttcacc ctgcctatata 120

acaaaaaaccc aattttgttc atattgaagc atgaaataaa tgagagcaag gttagggccaa 180

attaactctt gtggcacatgc cctaaaatgc cagttctaca ttgtgaaaa ttgtggtgcc 240

atgaatthaag atggatgact ggaaaaagggt gtggagaaa gagttaaaga tgaggaagag 300

atattttttag tatatgaagt tatccaggaa cttgatattc ataattcagt gctgtggaaa 360

tgaaaaaaaaat gattgaagag gtggAACGGA aatgaccta gggggaaaaaa aaaggaccaa 420

agaagtcgtta ttaaaatgtt aaatcgttat ttcgtaaattc aaattgtttt aatttccaaa 480

atagtcgtta aaggatctaa tagaaccaga attatttggg tgaattctgc aggtttatgt 540

ggcttgcac aacgtgttgg gctggaaatgtt atattaccaa atggaaattt ccattgttgg 600

ttttgctag tcccacccca attttagcctt aatggcgtt aaacgcgtt tggttggaaat 660

tgttccattt ccatgtgttc tgaattcagc tcatactccca gcatatagat atatcctcct 720

ttaactccgtt ccagaaccctt tcttcctgtt gcactccccca cccatagacc ttcatgtttt 780

ctccccacacc ctggatctca ctctcctctt agtaacagag acactccgtt ggttggactt 840

ccttgctttt ctctacttcc aaatcacaat ttcttacaac caagctttgt gctcccgagt 900

aaggcaggat gtacttagggg aatgtaaaac tgcaaactta aaaacctgca tcttcttggaa 960

gcacatgttt tacttaccaa atggttttaga gtcataagat gacctatttt tatataaaaag 1020

ttatattata gaataaaatg ttcatacgca tagactgttta agataaaaaaa ataggraatc 1080

ttgcaaggta attcttattt gcaagtgggt tatgtgttca ctctcctcta cctttatggt 1140

attttgggtt tcacttacga agcatacaac tagaaccata tccaaggcaga ctctgggttg 1200

ctgttaaccc agggcctaga ctcttagtgc ctctgaggca gaaccaaagg agcctgcact 1260

gggggaaatc ccttttctgtt cctgcctgtc tgccgtgtac ctgtgtacgtt attacaggct 1320

ttaggaccag ctgattgttta tgcttgcagg atggttttga aacagaaaca atacttgttt 1380

actgttagaa tcctatattt attattttc agtcctgtga atgctgtgaa aagatttatt 1440

cctttgaggc caggaagctc ccaggcatat atgcttctag gttaggattg tcctgactca 1500

ctaaagatgc caggatattg gggctgaggg gagtttgagg tgtt . . . 1544

〈210〉 130

211 <211> 508

<212> DNA

<213> Homo sapiens

〈400〉 130

tgaaatcagg gctggagctt tacttaggt tcacatggcc tccttaggaac catgggacaa 60

atggaaaca gtttatcggtt ggattcatga agtcagttagt agtaattgct tctttttgc 120

gggtgaactg aatgtatttc ttcaccaaat cttgatgtta acaattaaaa agaagaatg 180

acatgcaagt aggtcttagc agaaaaatgc aggctggca tgagtcatgt tgttaccctc 240

ccacatgctc ctacaatcca cagagatgcc tgtctgcagg ttcttgaagt tattgttagt 300

atttggtatac tcaaattttt cgtcactgtt cacatgccac ttctctgtg cacagtggtt 360

tcctcatttgccttttaacc tacactgagg agtctttgtc aggttgtcact gattttccaa 420

ttctgcagta atgagtaagc tcacggcatg gggaaagaaga cagtcagtcc aatgaagttc 480

tctaaattat tttaacattg cctttgaa

508

<210> 131

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (50)

<223> g or t

<220>

<221> unsure

<222> (54)

<223> g or c

<220>

<221> unsure

<222> (300)

<223> g or c

<220>

<221> unsure

<222> (407)

<223> g or a

<220>

<221> unsure

<222> (415)

<223> a, c, g or t

<220>

<221> unsure

<222> (417)

<223> g or c

<220>

<221> unsure

<222> (419)

<223> t or c

<220>

<221> unsure

<222> (430)

<223> a or t

<220>

<221> unsure

<222> (448)

<223> t or c

<220>

<221> unsure

<222> (449)

<223> g or t

<220>

<221> unsure

<222> (472)

<223> a, c, g or t

<400> 131

ggccctggc aattgcctc aagatgggg tttgaaaata acttacck actsaaggag 60
tgtctggagc acctccagt ctaagtctgc aagctccagt tcttgctaa aaccatgcca 120
gtggccaccc ttgggcttag acagctctgg gcctttgac cacaagccag cccctcgccc 180
tctctgtggc atagtcctct ctgccccagg actgcagggc ggcttcctcc aaggcttcca 240
aggctcaaaa gaaatttggc tccatccaag aaggctccag ctcccctact ggcccttggs 300
ttcaggccca cacccctggg ccagggccag agagtgtgtc tcaggagaat tcaatggct 360
ctagagagac acacagaaag tttggcatt tggaaattt tcaaggrtgt atgtntsgyt 420
cacgtatggw gcaggttgtc ctggtccykg ggtgcaggga agtggctgc anggaagtgg 480
atggagggg agcttgagga atataaggag cgggggtgga gactcaggct atggacaagg 540
acagccccaa ggttggaaag acctggcctt agtcgtcctc agcctagggg cagggcagtg 600
aagaaagctc tccccgtcc tgctgtaatg acccagagta gcctccccag gccggcatct 660
tatgtgtgtc ttccaccatc ctcatggtgg cactttcta ggcctgtctc ccagcaltgt 720
gcaaggctcg gaagagaacc aggaagtga aactgggtga aaacagaaag clcaatggat 780

gggctaggtt ccccagatca ttagggcaga gtttgcacgt cctctggta cttggaaatcca 840

cccgccccac gaatcatctc cctcttgaag gattttattt ctactggtt ttggaaacaaa 900

cicctgctga gaccccacag ccagaaactg aaagcagcag ctccccaaag cctggaaaat 960

ccctaagaga aggcctgggg caggaagtggtt agtgcacagg gacaggtt gagaaggggg 1020

cccaatggcc agggagtgaa ggaggtggcg ttgctgagag cagtctgcac atgcttctgt 1080

ctgagtgca gaaagggttc cagggtcgaa attacacttc tcgtacactgg agacgctgtt 1140

tgtgggagca ctgggtcat gcctggcaca caataggict gcaataaaacc atggtaaat 1200

cctg 1204

<210> 132

<211> 508

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (223)

<223> a, c, g or t

<220>

<221> unsure

<222> (237)

<223> a, c, g or t

<220>

<221> unsure

<222> (380)

<223> a, c, g or t

<220>

<221> unsure

<222> (468)

<223> a, c, g or t

<400> 132

cccgggagaa tcacttcagc ctgggagatc aaggctgcag tgagctctga acgcaccact 60

acactccagc ctgggtgaca gagtgagatc ctgtctcaa aaaagagaaa gaaaacctt 120

gagatttttc cattttaga gctgagagag cacttgtgaa acacacacac atgcacaaac 180

atataaacat gcatacaggc atgcacatgc acacacaaat acncatacac acacacnac 240

acacacacac caccaccacc atcatcagag gaacctacag aaaaggggac atttatagat 300

tccttaggaat atgccaaagc tttcaaaagc ctctatggac agctcattcc ttaactttc 360

ctctttaaaa tcttttttgc cttttttttt gccccagcca ctatcactgc ctctaggcagc 420

tgcaacgtta aacaatggcc actgattact ttcaacaaat aacctcanag aaaaggcgt 480

gtgtattgaa tggtatcaa gtcacgtc 508

<210> 133

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (313)

<223> a, c, g or t

<220>

<221> unsure

<222> (336)

<223> g or c

<220>

<221> unsure

<222> (401)

<223> g or c

<400> 133

gtcgactcga gcggccgcgg accgtttttt tttttttctt ctccctgtcc ctttctaata 60

tcttggagag ggttggagac tgaagagtga gtttggtctt ccacttgatc caggttctta 120

ttttgtttt ctacttcaaa gcgagaacctt ggtactgtga ctttgataag aattgacttc 180

aggcccagca agatccctca tgccgtaat cccagcactt tggggggcca aggaggagg 240

attgcgtgag cccaggagtt cgagacccac ctggcaaca tagggacctt gtctctacaa 300

aaaataaaat tanctgggtt tcatggtgca catcastggt cctggctact cgggaggcca 360

aggtgggagg aatgcgttag gatcgaggat caaggctgca stgagccat attgtgccac 420

tgcattccag cctggcaac agagtgagac actgtcttaa aaaaaaaaaa aaaaaacggt 480

ccgc 484

<210> 134

<211> 605

<212> DNA

<213> Homo sapiens

<400> 134

gctgcgtgtc taaaattaca tggagttgt gtctattttt tttccccctt tgcagcaact 60

tacacagcat ttttaacacc tttttttctt agttttttt ttcgggtttt tttccatca 120

ggaatttgag ttctctctaa cccagcttac tgtggacat aggaaaactc agtagaaata 180

ccttttgtga tcttgtttag ttttaagtctg atcttgtatct taaactcagt aagccactat 240

ctgcaattti gtacattata tagtattttt aagatatgga accttatgaa aaaaaaatag 300

caaatttagttt ctttttcccc cagaggggaa agttatgttc tgcaaatagt gtgtgtctta 360

tttactgtt gaacagcaat tgctatTTT tttttatgg cctagaactt caacatgtg 420

tatAGGAATC CTGTAgtGCC ACTAGTTAA TGCCGAATTc TCACTGGAT GTTACCATCA 480

aACATCAGTA CACTTGTcat TTCAcATGTG TTTAATGTGA CAGTTTTCA GTACTGTATG 540

TGTTAATTc TACTTTTTT AATATTTAA ATTGCTTTA AATAAACATA TTCTCAGTg 600

atccc 605

<210> 135

<211> 1786

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(151)

<220>

<221> unsure

<222> (689)

<223> g or a

<400> 135

g gca cga ggg tcc tct gca tgg ggt cag gtg ctt ctg tgc ttg ctg tcc 49

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

tac ctc tct cca cag cag ggc tct caa aac cat ttt gat ccc cca ttg 97
Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu
20 25 30
gca gag ggt tcc cct ctt tac aga gtt cag tca tta aaa gca tgg atc 145
Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile
35 40 45
agc tgt taatctcatt ggaggaggga acttgttctt gcattcattc atctggaaac 201
Ser Cys
50
cttcttgagt agccactgtc tgccagccac tgctcttagag atggaaaac agcacggaac 261
aaaaccaagg tccttcctcc agcgaattta tatccttcag gaagctggtt cctgccacca 321
acttagcagg caacagltct cctcccctag tggcacagg gtaccagtt ttagaaaa 381
gtggtccagc aaaggaagaa agcagaccaa cccagctgcc ttaccttatt ctggggccat 441
tccccagcg atgagagctg ctcttgttc tactgccacc atctctctg gctgcacttc 501
acctgctgct tgagctctg accttccttc agttccacca aatgaggaca ggaaatagca 561
gtcaagaccc ctggccctcg ctgagcgtga aacaggaagg caatggatg agttgctgg 621
acggaagaat gggctgggg cagaacaaat agggagcatt taaaagcttc tggctgataa 681
atctccargg tgcattccgg ttgccacgcc tgccccatt aaccigctcc tggtaataac 741
tgatccagca gctgctccag gagaggccgt cttttttc ccagccacgc tgcgttttgc 801
catgagactc cttgggcct gggcacagag agaaaagaat tgagactcag gaggctcagt 861
gggtgagaaa atgcaaagtg gcttcacaga cacaggctg tggagcaga tcgacgggaa 921
acttgggaga tgaacttcag ggccttccga cgccttgc tggatcataatg ctttggaaaa 981
aatggtagca tccttccat aactcagtct ctctcccta gtttccctga agtgcgtacgt 1041
tttagtatct ggagctcagt gatccccatg aatgaggat aaagttcac tcttggtatt 1101
ttcttaactag tgcttagggaa agtcctgaga cacgatcaca gccactgctt ggcatacagg 1161
gcctccaccc aataagcaaa ctggagattc ctcagccctt cgtggacacc cacatctcat 1221

tcttctcaca gcagagaagc tc tcccttca gc ctgagctg tcttcttctt gc tg cagtgc 1281
 agcctgctcc ctcc tacccct ggcc tcaagg aagg tggaa acat tttctg catt caaag 1341
 tcctcacttt gacttatttg gc ctcatct tggc alggaa ggtggcaggc agaatggaaa 1401
 tacccccc caaaca aac agatattctt gc g tgtaa gggcagaagg gacaaggctct 1461
 ctatcccatg agacttagggg ccggagccca cctgccttcc cccacaactt ttcc tgc tca 1521
 aacc cactcc tctt gacaca ctggaatctg tattataat attttaaga aaatacaatg 1581
 atgg t gtc t gttt gttt gttt acagg t gttt gggaa taaaaactgt aagaaaatta 1641
 agtatttaaa atgttccaat aaagtgggt tttt gttt tctaataat tattgtgtac 1701
 ctattgtaaa tatgaaacac tcctat tttg caagctgagg acacaattt gttt tactgtt 1761
 atatataa ataa aagtttact gaatt 1786

<210> 136

<211> 50

<212> PRT

<213> Homo sapiens

<400> 136

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1	5	10	15
---	---	----	----

Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

20	25	30
----	----	----

Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

35	40	45
----	----	----

Ser Cys

50

<210> 137

<211> 835

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (535)..(729)

<400> 137

gaaaaatctc attatttcaa aatgatagac atataccaaa aacaagtcta taatgtgagt 60
agttactaaa atttacacat cttaaaagtg tgtaaatgct taaatttcag aattaccatc 120
agaacctcaa ttgacattcc tttgaatagg ctaataagtg acaaataaga ttaataagat 180
tttcaaaat cgccaggact ggtgaatata aatgatgatt gaactggaat aatattgggg 240
accaaataa atgaatgatt aaattatgaa gctcatatcc tttgaaggt agttgcaaag 300
agacatttca aaactgccct aggccattgc agcatccctt gatggcacgc ataatcatta 360
ccttaaagca tcaccactca tttgaccat atagattttt ttatgttagt taaaaggc 420
aatcagcctc atgactttat agttatgtct tgtatttaaa aacatttttt atacatttgg 480
ttatgttagt aaaccaaaaaa catttgatta ataaaatatc tatttgaata aatt atg 537

Met

1

agc tat cct ttc aaa cag cta ttg gca agt ttt aaa ccc aaa ata tat 585

Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile Tyr

5

10

15

aca cat agt tct gta ata aaa ctg ttt gac ttc tca agt aac atg act 633

Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met Thr

20

25

30

tcc tta ttt ctg aac agt act ggt tac ttt caa aat gaa ttt tta ttg 681

Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu Leu

35

40

45

aga ttt tcc att aac tat ttt ttt caa aga ctc aaa ttt tgt acc aag 729

Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr Lys
50 55 60 65
taaatccagg ctttatgtac aaacatgttg ttgttttat ttggggctgg gggaggtata 789
tgcgtgacag acttcctcgga attcataata aattttctaa aagcct 835

<210> 138

<211> 65

<212> PRT

<213> Homo sapiens

<400> 138

Met Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile

1 5 10 15

Tyr Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met

20 25 30

Thr Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu

35 40 45

Leu Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr

50 55 60

Lys

65

<210> 139

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(201)

<220>

<221> unsure

<222> (348)

<223> t or c

<220>

<221> unsure

<222> (353)

<223> a or t

<220>

<221> unsure

<222> (358)

<223> a or t

<220>

<221> unsure

<222> (363)

<223> a or t

<220>

<221> unsure

<222> (368)

<223> g or a

<400> 139

tgt ttc agt gtg act gtc ttg tta gag gtg aag ttt atc cag ggt aac 48

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1

5

10

15

ttg ctc act aac tat tcc ttt tta tgg cct ggg gtt aaa ggg agc atg 96

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met
 20 25 30
 gct cac act ggt gaa aat aag gaa ggc ctg gtc tta tct tgt att aat 144
 Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn
 35 40 45
 aat act ggc tgc att cca cca gcc aga gat ttc tat ctg cga aga cct 192
 Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro
 50 55 60
 atg aaa cac tgaagagaaa tgttaggcaga aggaaatggc cacatatacac 241
 Met Lys His
 65
 aagttctatt atatattctt ttgttaatac atattgtata ttacttgat gttttcttat 301
 atcatttact gtcttttga gttaatgtca gttttactc tctcaaytta cwatgtwaca 361
 twgtaartaatacataatgtcc ttatattat atatthaagc atctaacata tagagtttt 421
 ttcatataag tttaagataa atgtcaaaaa tatatgttct ttgttttc ttgctttaa 481
 aattatgtat ctttccctt tctttttt aagaataatt tattgttcag gagaaagaat 541
 gtatatgtaa ctgaaactat ctgaaatg cacattgaag gccgtgaggt actgataaac 601
 taaagaattt attattcaaa atact 626

<210> 140

<211> 67

<212> PRT

<213> Homo sapiens

<400> 140

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1 5 10 15

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

20 25 30

Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn

35 40 45

Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro

50 55 60

Met Lys His

65

<210> 141

<211> 525

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(525)

<400> 141

aagaaatgga ggactcagaa ccaaggattt ccaagtgtt tcttccaaag cacaggaatc 60

tcactctgtt aaagctggtc ttttctaact gagatgacag tc atg tcc ctt tcc 114

Met Ser Leu Ser

1

agg gac ctc aag gac gac ttt cac agt gac acg gta ctc tcc atc tta 162

Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val Leu Ser Ile Leu

5 10 15 20

aat gag cag cgc att cgg ggc att tta tgc gat gtc act atc att gtg 210

Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val Thr Ile Ile Val

25 30 35

gaa gat acc aaa ttt aaa gcc cat agc aat gtt ctg gca gct tca agc 258

Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu Ala Ala Ser Ser
40 45 50
ctg tat ttt aaa aat atc ttt tgg agc cat aca atc tgt att tcc agc 306
Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile Cys Ile Ser Ser
55 60 65
cac gtc ctg gag ctg gac gat ctc aaa gct gaa gtg ttt act gaa ata 354
His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val Phe Thr Glu Ile
70 75 80
ctt aat tat atc tac agt tcc aca gtc gtt gtc aag aga cag gaa aca 402
Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys Arg Gln Glu Thr
85 90 95 100
gtc act gat ctc gca gct gca gga aaa aag ctg gga ata tcg ttc ttg 450
Val Thr Asp Leu Ala Ala Gly Lys Lys Leu Gly Ile Ser Phe Leu
105 110 115
gaa gac ctt act gat cgc aac ttc tca aat tcc ccg ggt ccc tat gta 498
Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro Gly Pro Tyr Val
120 125 130
ttc tgt att act gaa aag gga gtg gtt 525
Phe Cys Ile Thr Glu Lys Gly Val Val
135 140

<210> 142

<211> 141

<212> PRT

<213> Homo sapiens

<400> 142

Met Ser Leu Ser Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val

1 5 10 15

Leu Ser Ile Leu Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val

20 25 30

Thr Ile Ile Val Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu

35 40 45

Ala Ala Ser Ser Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile

50 55 60

Cys Ile Ser Ser His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val

65 70 75 80

Phe Thr Glu Ile Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys

85 90 95

Arg Gln Glu Thr Val Thr Asp Leu Ala Ala Gly Lys Lys Leu Gly

100 105 110

Ile Ser Phe Leu Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro

115 120 125

Gly Pro Tyr Val Phe Cys Ile Thr Glu Lys Gly Val Val

130 135 140

<210> 143

<211> 1827

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138)..(1307)

<400> 143

gagacttggg ctggagccgc cctgggtgtc agcggctcggtccccgcga cgctccggcc 60

gtcgcgcagc ctcggcacct gcaggtccgt gcgccccg gctggcgccc ctgactccgt 120
 cccggccagg gagggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac 170
 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn
 1 5 10

ttg ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc teg 218
 Leu Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser
 15 20 25

cgg gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg 266
 Arg Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val
 30 35 40

gag gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag 314
 Glu Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu
 45 50 55

gtg tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc 362
 Val Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe
 60 65 70 75

aaa cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc 410
 Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val
 80 85 90

aca aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg 458
 Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg
 95 100 105

aac ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc 506
 Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro
 110 115 120

tac agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc 554
 Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly

125 130 135
cac agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct 602
His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro
140 145 150 155
cca tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc 650
Pro Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr
160 165 170
ctg agc tgc cag tct cca agg agt aag cct gct gtc caa tac cag tgg 698
Leu Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp
175 180 185
gat cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat 746
Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp
190 195 200
gtc atc cgt ggg tct tta agc ctc acc aac ctt tcg tct tcc atg gct 794
Val Ile Arg Gly Ser Leu Ser Ieu Thr Asn Leu Ser Ser Ser Met Ala
205 210 215
gga gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt 842
Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys
220 225 230 235
aat gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct 890
Asn Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala
240 245 250
gga gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg 938
Gly Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Ala Gly Leu
255 260 265
gtc ctc ttg tac cac cgc cggt ggc aag gcc ctg gag gag cca gcc aat 986

Val Leu Leu Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn
 270 275 280
 gat atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag 1034
 Asp Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys
 285 290 295
 agc tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc 1082
 Ser Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser
 300 305 310 315
 gca cga gcc ctc tgg cca ccc cat ggc cct ccc agg cct ggt gca ttg 1130
 Ala Arg Ala Leu Trp Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu
 320 325 330
 acc ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg 1178
 Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu
 335 340 345
 ccc acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt 1226
 Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly
 350 355 360
 ggg gtt tct tcc tct ggc ttt agc cgc atg ggt gct gtg cct gtg atg 1274
 Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met
 365 370 375
 gtg cct gcc cag agt caa gct ggc tct ctg gta tgatgacccc accactcatt 1327
 Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val
 380 385 390
 ggctaaaggaa tttgggtct ctccttccta taagggtcac ctcttagcaca gaggcctgag 1387
 tcatggaaaa gagtcacact cctgaccctt agtactctgc ccccacctct ctttactgtg 1447
 ggaaaaccat ctcagtaaga cctaagtgtc caggagacag aaggagaaga ggaagtggat 1507
 ctggaatgg gaggagccctc caccaccccc tgactccctcc ttatgaagcc agctgctgaa 1567

attagctact caccaagagt gaggggcaga gacttccagt cactgagtct cccaggcccc 1627
cttgatctgt accccacccc tatctaacad cacccttggc tcccaactcca gtcctcgta 1687
ttgatataac ctgtcaggct ggcttggtta ggtttactg gggcagagga taggaaatct 1747
cttattaaaaa ctaacatgaa atatgtgttg tttcatttg caaatttaaa taaagataca 1807
taatgtttgt atgagataag 1827

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1 5 10 15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln

20 25 30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val

35 40 45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln

50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys

65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg

100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val

115 120 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
130 135 140

Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
145 150 155 160

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
165 170 175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
180 185 190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
195 200 205

Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
210 215 220

Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
225 230 235 240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
245 250 255

Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
260 265 270

Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
275 280 285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Trp
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly

340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser

370 375 380

Gln Ala Gly Ser Leu Val

385 390

<210> 145

<211> 3466

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84)..(2726)

<400> 145

tgcgggaagc gatgttagtagt ctgccaggct gtccccggcc ctgcccggcc cgagccccgc 60

ggcccgccgc cggccaccgccc gcc atg aag aag cag ttc aac cgc atg aag cag 113

Met Lys Lys Gln Phe Asn Arg Met Lys Gln

1 5 10

ctg gct aac cag acc gtg ggc aga gct gag aaa aca gaa gtc ctt agt 161

Leu Ala Asn Gln Thr Val Gly Arg Ala Glu Lys Thr Glu Val Leu Ser

15 20 25

gaa gat cta tta cag att gag aga cgc ctg gac acg gtg cgg tca ata 209

Glu Asp Leu Leu Gln Ile Glu Arg Arg Leu Asp Thr Val Arg Ser Ile

30 35 40

tgc cac cat tcc cat aag cgc ttg gtg gca tgt ttc cag ggc cag cat 257
Cys His His Ser His Lys Arg Leu Val Ala Cys Phe Gln Gly Gln His
45 50 55
ggc acc gat gcc gag agg aga cac aaa aaa ctg cct ctg aca gct ctt 305
Gly Thr Asp Ala Glu Arg Arg His Lys Lys Leu Pro Leu Thr Ala Leu
60 65 70
gct caa aat atg caa gaa gca tcg act cag ctg gaa gac tct ctc ctg 353
Ala Gln Asn Met Gln Glu Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu
75 80 85 90
ggg aag atg ctg gag acg tgt gga gat gct gag aat cag ctg gct ctc 401
Gly Lys Met Leu Glu Thr Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu
95 100 105
gag ctc tcc cag cac gaa gtc ttt gtt gag aag gag atc gtg gac cct 449
Glu Leu Ser Gln His Glu Val Phe Val Glu Lys Glu Ile Val Asp Pro
110 115 120
ctg tac ggc ata gct gag gtg gag att ccc aac atc cag aag cag agg 497
Leu Tyr Gly Ile Ala Glu Val Glu Ile Pro Asn Ile Gln Lys Gln Arg
125 130 135
aag cag ctt gca aga ttg gtg tta gac tgg gat tca gtc aga gcc agg 545
Lys Gln Leu Ala Arg Leu Val Leu Asp Trp Asp Ser Val Arg Ala Arg
140 145 150
tgg aac caa gct cac aaa tcc tca gga acc aac ttt cag ggg ctt cca 593
Trp Asn Gln Ala His Lys Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro
155 160 165 170
tca aaa ata gat act cta aag gaa gag atg gat gaa gct gga aat aaa 641
Ser Lys Ile Asp Thr Leu Lys Glu Glu Met Asp Glu Ala Gly Asn Lys
175 180 185

gta gaa cag tgc aag gat caa ctt gca gca gac atg tac aac ttt atg		689	
Val Glu Gln Cys Lys Asp Gln Leu Ala Ala Asp Met Tyr Asn Phe Met			
190	195	200	
gcc aaa gaa ggg gag tat ggc aaa ttc ttt gtt acg tta tta gaa gcc		737	
Ala Lys Glu Gly Glu Tyr Gly Lys Phe Phe Val Thr Leu Leu Glu Ala			
205	210	215	
caa gca gat tac cat aga aaa gca tta gca gtc tta gaa aag acc ctc		785	
Gln Ala Asp Tyr His Arg Lys Ala Leu Ala Val Leu Glu Lys Thr Leu			
220	225	230	
ccc gaa atg cga gcc cat caa gat aag tgg gcg gaa aaa cca gcc ttt		833	
Pro Glu Met Arg Ala His Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe			
235	240	245	250
ggg act ccc cta gaa gaa cac ctg aag agg agc ggg cgc gag att gcg		881	
Gly Thr Pro Leu Glu Glu His Leu Lys Arg Ser Gly Arg Glu Ile Ala			
255	260	265	
ctg ccc att gaa gcc tgt gtc atg ctg ctt ctg gag aca ggc atg aag		929	
Leu Pro Ile Glu Ala Cys Val Met Leu Leu Leu Glu Thr Gly Met Lys			
270	275	280	
gag gag ggc ctt ttc cga att ggg gct ggg gcc tcc aag tta aag aag		977	
Glu Glu Gly Leu Phe Arg Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys			
285	290	295	
ctg aaa gct gct ttg gac tgt tct act tct cac ctg gat gag ttc tat		1025	
Leu Lys Ala Ala Leu Asp Cys Ser Thr Ser His Leu Asp Glu Phe Tyr			
300	305	310	
tca gac ccc cat gct gta gca ggt gct tta aaa tcc tat tta cgg gaa		1073	
Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu			

315	320	325	330	
ttg cct gaa cct ttg atg act ttt aat ctg tat gaa gaa tgg aca caa				1121
Leu Pro Glu Pro Leu Met Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln				
335	340	345		
gtt gca agt gtg cag gat caa gac aaa aaa ctt caa gac ttg tgg aga				1169
Val Ala Ser Val Gln Asp Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg				
350	355	360		
aca tgt cag aag ttg cca cca caa aat ttt gtt aac ttt aga tat ttg				1217
Thr Cys Gln Lys Leu Pro Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu				
365	370	375		
atc aag ttc ctt gca aag ctt gct cag acc agc gat gtg aat aaa atg				1265
Ile Lys Phe Leu Ala Lys Leu Ala Gln Thr Ser Asp Val Asn Lys Met				
380	385	390		
act ccc agc aac att gcg att gtg tta ggc cct aac ttg tta tgg gcc				1313
Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Ala				
395	400	405	410	
aga aat gaa gga aca ctt gct gaa atg gca gca gcc aca tcc gtc cat				1361
Arg Asn Glu Gly Thr Leu Ala Glu Met Ala Ala Ala Thr Ser Val His				
415	420	425		
gtg gtt gca gtg att gaa ccc atc att cag cat gcc gac tgg ttc ttc				1409
Val Val Ala Val Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe				
430	435	440		
cct gaa gag gtg gaa ttt aat gta tca gaa gca ttt gta cct ctc acc				1457
Pro Glu Glu Val Glu Phe Asn Val Ser Glu Ala Phe Val Pro Leu Thr				
445	450	455		
acc ccg agt tct aat cac tca ttc cac act gga aac gac tct gac tcg				1505
Thr Pro Ser Ser Asn His Ser Phe His Thr Gly Asn Asp Ser Asp Ser				

460 465 470
ggg acc ctg gag agg aag cgg cct gct agc atg gcg gtg atg gaa gga 1553
Gly Thr Leu Glu Arg Lys Arg Pro Ala Ser Met Ala Val Met Glu Gly
475 480 485 490
gac ttg gtg aag aag gaa agc ttt ggt gtg aag ctt atg gac ttc cag 1601
Asp Leu Val Lys Lys Glu Ser Phe Gly Val Lys Leu Met Asp Phe Gln
495 500 505
gcc cac cgg cgg ggt ggc act cta aat aga aag cac ata tcc ccc gct 1649
Ala His Arg Arg Gly Gly Thr Leu Asn Arg Lys His Ile Ser Pro Ala
510 515 520
ttc cag ccg cca ctt ccg ccc aca gat ggc agc acc gtg gtg ccc gct 1697
Phe Gln Pro Pro Leu Pro Pro Thr Asp Gly Ser Thr Val Val Pro Ala
525 530 535
ggc cca gag ccc cct ccc cag agc tct agg gct gaa agc agc tct ggg 1745
Gly Pro Glu Pro Pro Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly
540 545 550
ggt ggg act gtc ccc tct tcc gcg ggc ata ctg gag cag ggg ccg agc 1793
Gly Gly Thr Val Pro Ser Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser
555 560 565 570
cca ggc gac ggc agt cct ccc aaa ccg aag gac cct gta tct gca gct 1841
Pro Gly Asp Gly Ser Pro Pro Lys Pro Lys Asp Pro Val Ser Ala Ala
575 580 585
gtg cca gca cca ggg aga aac aac agt cag ata gca tct ggc caa aat 1889
Val Pro Ala Pro Gly Arg Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn
590 595 600
cag ccc cag gca gct gct ggc tcc cac cag ctc tcc atg ggc caa cct 1937

Gln Pro Gln Ala Ala Ala Gly Ser His Gln Leu Ser Met Gly Gln Pro
605 610 615
cac aat gct gca ggg ccc agc ccg cat aca ctg cgc cga gct gtt aaa 1985
His Asn Ala Ala Gly Pro Ser Pro His Thr Leu Arg Arg Ala Val Lys
620 625 630
aaa ccc gct cca gca ccc ccg aaa ccg ggc aac cca cct cct ggc cac 2033
Lys Pro Ala Pro Ala Pro Pro Lys Pro Gly Asn Pro Pro Pro Gly His
635 640 645 650
ccc ggg ggc cag agt tct tca gga aca tct cag cat cca ccc agt ctg 2081
Pro Gly Gly Gln Ser Ser Gly Thr Ser Gln His Pro Pro Ser Leu
655 660 665
tca cca aag cca ccc acc cga agc ccc tct cct ccc acc cag cac acg 2129
Ser Pro Lys Pro Pro Thr Arg Ser Pro Ser Pro Pro Thr Gln His Thr
670 675 680
ggc cag cct cca ggc cag ccc tcc gcc ccc tcc cag ctc tca gca ccc 2177
Gly Gln Pro Pro Gly Gln Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro
685 690 695
cgg agg tac tcc agc agc ttg tct cca atc caa gct ccc aat cac cca 2225
Arg Arg Tyr Ser Ser Ser Leu Ser Pro Ile Gln Ala Pro Asn His Pro
700 705 710
ccg ccg cag ccc cct acg cag gcc acg cca ctg atg cac acc aaa ccc 2273
Pro Pro Gln Pro Pro Thr Gln Ala Thr Pro Leu Met His Thr Lys Pro
715 720 725 730
aat agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga 2321
Asn Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly
735 740 745
ctt gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt 2369

Leu Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser
 750 755 760
 act ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc 2417
 Thr Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr
 765 770 775
 ctg gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta 2465
 Leu Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu
 780 785 790
 ccg aga ccg aga cca gta cca aag cca agg aac cgg ccc agc gtg ccc 2513
 Pro Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro
 795 800 805 810
 cca ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc ctc 2561
 Pro Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu
 815 820 825
 acc aac aca gca cca aca gct tcc aag ata gta aca gac tcc aat tcc 2609
 Thr Asn Thr Ala Pro Thr Ala Ser Lys Ile Val Thr Asp Ser Asn Ser
 830 835 840
 agg gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac 2657
 Arg Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp
 845 850 855
 tca gcc agc aaa gac gtg cct ggc cgc atc ctg ctg gat ata gac aat 2705
 Ser Ala Ser Lys Asp Val Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn
 860 865 870
 gat acc gag agc act gcc ctg tgaagaaagc cctttcccgag ccctccacca 2756
 Asp Thr Glu Ser Thr Ala Leu
 875 880

cttccacctt ggcgagtgga gcagggcag gcgaacctt ttcgttgtcaccgaaacagt 2816
gaaaagcttt cagtgaggcaaaaggaggcctcactgtgcgggacctggccttcgtcac 2876
ggcccaagga gaacctggag gccaccactaaagctgaatg acctgtgtcttgaagaagtt 2936
ggctttcttt acatgggaag gaaatcatgc caaaaaaaatc caaaacaaag aagtacctgg 2996
agtggagaga gtattccgtc tgaaacgcgc ataggaagctttgtccctgtgttaatgc 3056
ggcagcacc tacagcaact tggaaatgagt aagaagcagt gcgttaactatctatttaat 3116
aaaatgcgtt cattatgcaa gtcgcctact ctctgttacc tggacgttca ttcttatgtt 3176
tttaggaggga ggctgcgccttcagactt gctgcagaat catttgtatcatgtatgg 3236
ctgtgtctcc ccagtcctt cagaaccatg cccatggatg gtgactgctggctgtcac 3296
ctcatcaaac tggatgtgac ccatgccgcc tcgttggatt gtcggaatgt agacagaaat 3356
gtactgttctttttttttttttaaacaat gtaattgtca ctgtataagg accgaacatt 3416
attcttagttt catgttaat ttgaattaaa tatattctgt gglttatatg 3466

〈210〉 146

211 881

<212> PRT

<213> Homo sapiens

〈400〉 146

Met Lys Lys Gln Phe Asn Arg Met Lys Gln Leu Ala Asn Gln Thr Val

1 5 10 15

Gly Arg Ala Glu Lys Thr Glu Val Leu Ser Glu Asp Leu Leu Gln Ile

20 25 30

Glu Arg Arg Leu Asp Thr Val Arg Ser Ile Cys His His Ser His Lys

35 40 45

Arg Leu Val Ala Cys Phe Gln Gly Gln His Gly Thr Asp Ala Glu Arg

50 55 60

Arg His Lys Lys Leu Pro Leu Thr Ala Leu Ala Gln Asn Met Gln Glu

65	70	75	80
Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu Gly Lys Met Leu Glu Thr			
85	90	95	
Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu Glu Leu Ser Gln His Glu			
100	105	110	
Val Phe Val Glu Lys Glu Ile Val Asp Pro Leu Tyr Gly Ile Ala Glu			
115	120	125	
Val Glu Ile Pro Asn Ile Gln Lys Gln Arg Lys Gln Leu Ala Arg Leu			
130	135	140	
Val Leu Asp Trp Asp Ser Val Arg Ala Arg Trp Asn Gln Ala His Lys			
145	150	155	160
Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro Ser Lys Ile Asp Thr Leu			
165	170	175	
Lys Glu Glu Met Asp Glu Ala Gly Asn Lys Val Glu Gln Cys Lys Asp			
180	185	190	
Gln Leu Ala Ala Asp Met Tyr Asn Phe Met Ala Lys Glu Gly Glu Tyr			
195	200	205	
Gly Lys Phe Phe Val Thr Leu Leu Glu Ala Gln Ala Asp Tyr His Arg			
210	215	220	
Lys Ala Leu Ala Val Leu Glu Lys Thr Leu Pro Glu Met Arg Ala His			
225	230	235	240
Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe Gly Thr Pro Leu Glu Glu			
245	250	255	
His Leu Lys Arg Ser Gly Arg Glu Ile Ala Leu Pro Ile Glu Ala Cys			
260	265	270	
Val Met Leu Leu Leu Glu Thr Gly Met Lys Glu Glu Gly Leu Phe Arg			
275	280	285	

Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys Leu Lys Ala Ala Leu Asp

290 295 300

Cys Ser Thr Ser His Leu Asp Glu Phe Tyr Ser Asp Pro His Ala Val

305 310 315 320

Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro Leu Met

325 330 335

Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln Val Ala Ser Val Gln Asp

340 345 350

Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg Thr Cys Gln Lys Leu Pro

355 360 365

Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu Ile Lys Phe Leu Ala Lys

370 375 380

Leu Ala Gln Thr Ser Asp Val Asn Lys Met Thr Pro Ser Asn Ile Ala

385 390 395 400

Ile Val Leu Gly Pro Asn Leu Leu Trp Ala Arg Asn Glu Gly Thr Leu

405 410 415

Ala Glu Met Ala Ala Ala Thr Ser Val His Val Val Ala Val Ile Glu

420 425 430

Pro Ile Ile Gln His Ala Asp Trp Phe Phe Pro Glu Glu Val Glu Phe

435 440 445

Asn Val Ser Glu Ala Phe Val Pro Leu Thr Thr Pro Ser Ser Asn His

450 455 460

Ser Phe His Thr Gly Asn Asp Ser Asp Ser Gly Thr Leu Glu Arg Lys

465 470 475 480

Arg Pro Ala Ser Met Ala Val Met Glu Gly Asp Leu Val Lys Lys Glu

485 490 495

Ser Phe Gly Val Lys Leu Met Asp Phe Gln Ala His Arg Arg Gly Gly
500 505 510
Thr Leu Asn Arg Lys His Ile Ser Pro Ala Phe Gln Pro Pro Leu Pro
515 520 525
Pro Thr Asp Gly Ser Thr Val Val Pro Ala Gly Pro Glu Pro Pro Pro
530 535 540
Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly Gly Gly Thr Val Pro Ser
545 550 555 560
Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser Pro Gly Asp Gly Ser Pro
565 570 575
Pro Lys Pro Lys Asp Pro Val Ser Ala Ala Val Pro Ala Pro Gly Arg
580 585 590
Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn Gln Pro Gln Ala Ala Ala
595 600 605
Gly Ser His Gln Leu Ser Met Gly Gln Pro His Asn Ala Ala Gly Pro
610 615 620
Ser Pro His Thr Leu Arg Arg Ala Val Lys Lys Pro Ala Pro Ala Pro
625 630 635 640
Pro Lys Pro Gly Asn Pro Pro Pro Gly His Pro Gly Gly Gln Ser Ser
645 650 655
Ser Gly Thr Ser Gln His Pro Pro Ser Leu Ser Pro Lys Pro Pro Thr
660 665 670
Arg Ser Pro Ser Pro Pro Thr Gln His Thr Gly Gln Pro Pro Gly Gln
675 680 685
Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro Arg Arg Tyr Ser Ser Ser
690 695 700
Leu Ser Pro Ile Gln Ala Pro Asn His Pro Pro Pro Gln Pro Pro Thr

705	710	715	720
Gln Ala Thr Pro Leu Met His Thr Lys Pro Asn Ser Gln Gly Pro Pro			
725	730	735	
Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu Glu Gln Pro Ser His			
740	745	750	
Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr Pro Pro Leu Gly Lys			
755	760	765	
Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu Ala Gly Gly Asn Pro			
770	775	780	
Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro Arg Pro Arg Pro Val			
785	790	795	800
Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro Pro Gln Pro Pro			
805	810	815	
Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr Asn Thr Ala Pro Thr			
820	825	830	
Ala Ser Lys Ile Val Thr Asp Ser Asn Ser Arg Val Ser Glu Pro His			
835	840	845	
Arg Ser Ile Phe Pro Glu Met His Ser Asp Ser Ala Ser Lys Asp Val			
850	855	860	
Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn Asp Thr Glu Ser Thr Ala			
865	870	875	880
Leu			

<210> 147

<211> 3021

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (140)..(1105)

<400> 147

gagctgccgc tgtcgcttt gcttcagccg cagtcgccac tggctgcctg aggtgcctt 60
 acagcctgtt ccaagtgtgg cttaatccgt ctccaccacc agatcttct ccgtggattc 120
 ctctgctaag accgcgtgcc atg cca gtg acg gta acc cgc acc acc atc aca 172

Met	Pro	Val	Thr	Val	Thr	Arg	Thr	Thr	Ile	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1		5			10					
---	--	---	--	--	----	--	--	--	--	--

acc acc acg acg tca tct tcg ggc ctg ggg tcc ccc atg atc gtg ggg 220

Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly

15		20		25						
----	--	----	--	----	--	--	--	--	--	--

tcc cct cggtgcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag 268

Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln

30		35		40						
----	--	----	--	----	--	--	--	--	--	--

ctg gtg tct acc tgc gtg gcc ttc tcg ctg gtg gct agc gtg ggc gcc 316

Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala

45		50	.	55						
----	--	----	---	----	--	--	--	--	--	--

tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc 364

Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys

60		65		70		75				
----	--	----	--	----	--	----	--	--	--	--

ttc tcc gtg acc ctg atc atc ctc atc gtg gag ctg tgc ggg ctc cag 412

Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln

80		85		90						
----	--	----	--	----	--	--	--	--	--	--

gcc cgc ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc 460

Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys

95	100	105	
tat gcg ggc ctc ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc			508
Tyr Ala Gly Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr			
110	115	120	
tat gtc cag ttc ctg tcc cac ggc cgt tcg cgg gac cac gcc atc gcc			556
Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala			
125	130	135	
gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg			604
Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val			
140	145	150	155
gcc tgg acc cgg gcc cgg ccc ggc gag atc act ggc tat atg gcc acc			652
Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr			
160	165	170	
gta ccc ggg ctg ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc			700
Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile			
175	180	185	
ttc gcg ttc atc agc gac ccc aac ctg tac cag cac cag ccg gcc ctg			748
Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu			
190	195	200	
gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc			796
Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile			
205	210	215	
gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc			844
Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro			
220	225	230	235
ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat			892
Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Ser Val Leu Leu Tyr			

240

245

250

gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat 940

Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr

255

260

265

ggc ggc cag cct cgg cgc tcg aga gat gta agc tgc agc cgc agc cat 988

Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His

270

275

280

gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg 1036

Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu

285

290

295

acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc 1084

Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala

300

305

310

315

cac ctg gti ttt gtc aag gtc taagactctc ccaagaggct cccgttccct 1135

His Leu Val Phe Val Lys Val

320

ctccaacctc ttgttcttc ttgcccaggt ttctttatg gagtacttct ttccctccgcc 1195

tttcctctgt ttccctcttc ctgtctcccc tccctccac ctltttcttt ctttccaaat 1255

tcccttgact ctaaccagtt ctggatgca tcttcttcct tccctttctt ctgtgtgttt 1315

ccttcctgtg ttgtttgtt gccccacatcc tgggttccacc cctgagctgt ttcttttttt 1375

cttttcttcc tttttttttt ttttttaaga cggattctca ctctgtggcc caggctggag 1435

cgcagtggtg cgatctcgac tcactgcaac cccgcctcc tgggttcaag cgattctcct 1495

gccccagcct cccaaatgac tgggaggaca ggtgtgagct gcccaccca gcctgtttct 1555

ctttttccac tcttctttt tctcatctt tttctgggtt gcctgtggc tttcttatct 1615

gcctgttttg caagcacctt ctccctgttc ctgggagcc ctgagacttc tttctctct 1675

tgccctccacc caccccaaaa gggtgtgagc tcacatccac acccccttgcg ccgtccatg 1735

ccacagcccc ccaaggggcc ccatigccaa agcatgcctg cccaccctcg ctgtgcctta 1795
gtcagtgtgt acgtgtgtgt gtgtgtgtgt tgggggggtg ggggtgggt agctgggat 1855
tggccctct ttctcccagt ggaggaagggt gtgcagtgta cttccccttt aaattaaaaa 1915
acatatata atatataatgggatcagt aatttccaat gggcgggagg cattaagcac 1975
cgaccctggg tccctaggcc ccgcctggca ctcagccttg ccagagattg gctccagaat 2035
tttgcagg cttacagaac acccactgccc tagaggccat cttaaaggaa gcagggctg 2095
gatgccttgc atcccaacta ttctctgtgg tatgaaaaag aaaaaaaaaaaa aaaaagaagg 2155
agtccccccc gggcggtggt gctcacgcct gtaatcccag cactttggga gaccaagtca 2215
ggcaatca tgaagtcagg agttcaagac cagcctggcc aacatggtga aagcatgtct 2275
ctattaaaaa tacaaaaatt agccggcgt ggtggcggc gcctgtatac ccaggtatTTT 2335
ggggggactg agacaggaga atcccttcaa cccgggagggt ggaggttgca gtaagtcaag 2395
atggcaccac tgtgctccag cctgggggac agagcgagac tccatctcaa aaaaaaaaaagg 2455
gaatcggacg aagaaccaca ggatgttcaa gacaactgtc tgaagtatTTT gtgagggaca 2515
gcgatgtggc cctctgtgtt aagaataacg tgtccgttt tggcagagag aagaaaaatag 2575
ccactgcccc cttcaaggc aagatcgacc tttctgttt tgTTTgttt ttctttcttt 2635
ttccctggcca tgaggacaaa aattactgag tggcccttaa agaggaaagt ttgtttttag 2695
ctgttcttgc ttgcccgtag gtgggagggt ggggattgtc gcgccttagc tagaggaatg 2755
gctttgcttg aatgtgttagt gcacacgcac gggtgttct gtgtgttagt tgcttcttgc 2815
tgctgcttcc tgcttgcgt ggactcacat acataacgtg atatataat atatataataa 2875
atgtataat atatatTTTaa tttttttta aatccttgaa gcttctgttt cctatcagtt 2935
cctgttgtta atcgtagaac cggtgtccct tccccattc ccgtatccat catgttcttt 2995
ttcttttaaa tatcaatata aaaggt

3021

<210> 148

<211> 322

<212> PRT

<213> Homo sapiens

<400> 148

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Ser
1 5 10 15
Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala Leu
20 25 30
Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys
35 40 45
Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met
50 55 60
Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu
65 70 75 80
Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu
85 90 95
Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Gly Leu Phe
100 105 110
Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu
115 120 125
Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser
130 135 140
Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala
145 150 155 160
Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu
165 170 175
Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser
180 185 190
Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala
195 200 205

Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn
210 215 220
Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
225 230 235 240
Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val
245 250 255
Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg
260 265 270
Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys
275 280 285
Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu
290 295 300
Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val
305 310 315 320
Lys Val

<210> 149

<211> 4409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (39)..(2027)

<400> 149

ggtgtcagga tcgcagaaag tatgtccctt ctctcacc atg agc tgg ctc tcc agt 56

Met Ser Trp Leu Ser Ser

tcc cag gga gtg gta cta aca gcc tac cac ccc agc ggc aag gac cag	104		
Ser Gln Gly Val Val Leu Thr Ala Tyr His Pro Ser Gly Lys Asp Gln			
10	15	20	
gcc gtc ggg aac aac agc cat gca aag gca ggg gag gaa gcc acc tcg agt	152		
Ala Val Gly Asn Ser His Ala Lys Ala Gly Glu Glu Ala Thr Ser Ser			
25	30	35	
cgc aga tat ggc cag tac act atg aac cag gaa agc acc acc atc aaa	200		
Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln Glu Ser Thr Thr Ile Lys			
40	45	50	
gtt atg gag aag cct cca ttt gat cga tca att tcc cag gat tct ttg	248		
Val Met Glu Lys Pro Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu			
55	60	65	70
gat gaa cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc aag	296		
Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys			
75	80	85	
aaa tct agt gaa aac aac agc caa gaa gat caa gag gtg gtt gtt gtc aaa	344		
Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys			
90	95	100	
gag cct gat gag gga gaa ttg gaa gaa gag tgg ctt aaa gag gcc ggt	392		
Glu Pro Asp Glu Gly Glu Leu Glu Glu Trp Leu Lys Glu Ala Gly			
105	110	115	
tta tcc aat ctc ttc gga gag tct gct gga gat cca cag gaa agc att	440		
Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile			
120	125	130	
gtg ttt tta tca aca ttg acg cgg acc cag gca gca gca gtt cag aag	488		
Val Phe Leu Ser Thr Leu Thr Arg Thr Gln Ala Ala Val Gln Lys			

135	140	145	150
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac aaa cag tac			536
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn Lys Gln Tyr			
155	160	165	
cag att cct gac gtc aga gac ata ttt gct caa cag aga gaa tca aaa			584
Gln Ile Pro Asp Val Arg Asp Ile Phe Ala Gln Gln Arg Glu Ser Lys			
170	175	180	
gaa aca gct cca ggt ggc act gaa tcg cag tca ctt aga aca aat gaa			632
Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln Ser Leu Arg Thr Asn Glu			
185	190	195	
aac aaa tac caa gga aga gat gac gag gca tct aac ctt gtt ggt gaa			680
Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu			
200	205	210	
gag aag ctg atc cca cct gag gag acg cct gcc cct gaa aca gac atc			728
Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr Asp Ile			
215	220	225	230
aac ctg gag gta tca ttt gcc gag caa gca ctc aat cag aaa gag agc			776
Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu Asn Gln Lys Glu Ser			
235	240	245	
tcc aag gag aaa atc cag aag agc aaa ggc gat gat gcc aca tta cct			824
Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly Asp Asp Ala Thr Leu Pro			
250	255	260	
agt ttc aga ttg cca aaa gac aaa acg ggt acc aca agg att ggt gac			872
Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp			
265	270	275	
ctc gca ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att gag			920
Leu Ala Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile Glu			

280	285	290	
ctg act gcc ctc tat gat gta ttg ggt att gag ctg aaa caa caa aaa 968			
Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu Lys Gln Gln Lys			
295	300	305	310
gct gtg aaa atc aaa aca aaa gat tct ggt ctt ttt tgc gtt cca ttg 1016			
Ala Val Lys Ile Lys Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu			
315	320	325	
aca gcg cta tta gaa caa gat cag agg aaa gta cca gga atg cga ata 1064			
Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys Val Pro Gly Met Arg Ile			
330	335	340	
ccc ttg atc ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg 1112			
Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu			
345	350	355	
gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att aga atc aag 1160			
Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys			
360	365	370	
aat ctt tgc caa gaa cta gaa gca aag ttt tat gaa ggg act ttt aat 1208			
Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe Tyr Glu Gly Thr Phe Asn			
375	380	385	390
tgg gaa agt gtc aaa cag cat gat gcc gcc agc ctg ctg aag ctc ttc 1256			
Trp Glu Ser Val Lys Gln His Asp Ala Ala Ser Leu Leu Lys Leu Phe			
395	400	405	
att cgg gag ttg ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc 1304			
Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala			
410	415	420	
ttt cag gct gtc cag aat ctt cca acc aag aag cag caa cta cag gct 1352			

Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu Gln Ala
425 430 435
ttg aac ctt ctt ggc atc ctc cta cct gat gca aac agg gac aca ctg 1400
Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp Ala Asn Arg Asp Thr Leu
440 445 450
aag gcc ctt ctt gaa ttt ctc caa aga gta ata gat aat aaa gaa aaa 1448
Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile Asp Asn Lys Glu Lys
455 460 465 470
aat aaa atg aca gtc atg aat gta gca atg gtc atg gcc ccg aat ctc 1496
Asn Lys Met Thr Val Met Asn Val Ala Met Val Met Ala Pro Asn Leu
475 480 485
ttt atg tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa ttt 1544
Phe Met Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu Phe
490 495 500
gta atg gca gct ggg aca gca aat acc atg cac tta ttg att aag tac 1592
Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu Leu Ile Lys Tyr
505 510 515
caa aaa ctt ctg tgg aca att ccc aag ttt att gta aac caa gtg agg 1640
Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe Ile Val Asn Gln Val Arg
520 525 530
aag caa aac acg gaa aat cat aaa aag gat aaa aga gcc atg aag aaa 1688
Lys Gln Asn Thr Glu Asn His Lys Lys Asp Lys Arg Ala Met Lys Lys
535 540 545 550
ttg ctg aag aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat 1736
Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp
555 560 565
aag agt aca aat gat gct gac gtt cct cag gga gtg att cga gtg caa 1784

Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln
 570 575 580
 gct ccc cat ctt tcg aaa gtt tcc atg gca ata cag cta act gaa gaa 1832
 Ala Pro His Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu
 585 590 595
 cta aaa gcc agt gat gta ctt gcc agg ttt ctc agc caa gaa agt ggg 1880
 Leu Lys Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly
 600 605 610
 gtt gcc cag act ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga 1928
 Val Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly
 615 620 625 630
 gga aat att ggg gaa cgc tgc ctt gat gat gac act tac atg aag gat 1976
 Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys Asp
 635 640 645
 tta tat cag ctt aac cca aat gct gag tgg gtt ata aag tca aag cca 2024
 Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser Lys Pro
 650 655 660
 ttg tagaagactt aacaagctgc agataaccat gtggacttct gtcataattc 2077
 Leu
 ttgctgagtc aagagtgtaa ataaaagaaa tggcaggact catattttc agttgtaccc 2137
 aagtatcaa aaatgactct cttaaagcctt aaaaagtcat agatttgtgc tgctgccaga 2197
 attatattaa ttattattaa ttttattttt agaaaaaaaaa ttctggagt gagagtaaag 2257
 aggcttaatt agtttgtgg cagtttcat atgctctgt aaatgtgtcc agaigtgaca 2317
 tagttttttt tttttttaat atgtggaaat gtcttcctt cccattttt tctcctaaaa 2377
 tcataataac tgtaatatat gctcttcac ctcttattacc tcctcacatc tacccttcc 2437
 cagtttagtt tgcttttiga ccaaaaagat aacaaatacc aggtatggca agttgtgaag 2497

acagcacatt aaaacatacc taatitcaca gtaattccgt cacgacagaa tggtagtatt 2557
catctcttg aatcatttcgc tcaaataata acatccacc ttccctgct gtatcacagg 2617
aagtgatttg cattttttt cagttcatct gacttatgtt cacagaaccg tatcagcgac 2677
caagaaaata ggactgtcag aagctgccag ttattactga accattaaat acttatatac 2737
taagaataaa taaaatatac ccatgtgaaa taataatgg attatggata acaagagagt 2797
gaaagccaaa gcactttctg tctactglac tcttclaaat ggaattttaa aagtcatagc 2857
tggctttacg tggtagtattt attagcatta taaatacgca tgatagtata atccagtaat 2917
ggttgaagaa tgtatTTTAC ttaaagaggg atttttttt ttaagtcctg aataagtcta 2977
ctggaagaat tattttctg ggtgaaaagc ttttttttgt gttttttttt taaataatcg 3037
gagtcaattt attaaaatgt tcttgcattt actattccca gggattttaa tgcacaaacc 3097
atattgtgac aagagatgag cctctgtact gtaaataaga aatgaagtag agaaatgtt 3157
aatatTTTAT gagtttagaa tatagtaat aaaaggtgat gtaaatgaat gctgcacaaa 3217
cggtgttcat gatacttttta gtagtactttt aggaaaaact acacatttc agaagctttt 3277
gatgtctcta atgaaggggg ggaatgcgtg taatgagaac agtcataaat ttttagcata 3337
taattacaag aacagcctgt ggatatgatc actaaatga ttttggggg attcgtgcc 3397
ttgtttttt attaaaaga aaattttgtt attaaatgcc tttttctaaa ttatcttc 3457
tttggaatcat tactttat cctatgtgtt tatgagtatt tttgtttttt ttttattaaat 3517
attgagaaat ggactttttt gttttaaaa gtcacctcta ttttctattt tctttgtaat 3577
ttttaaagta ggaagatgtc agagatgtaa atatgtttc gtttttagtt ttttccccc 3637
tacaaatTTT Tatttttcag gatTTTcaaa atacagtttta gttttttctt ttgacaatata 3697
gtattttttt cccaaatttcg aaaatggtac ttattttgtt gttttttttt 3757
taaaagaaaa attaagtgtt taaaacattt taggagtata caacttc 3817
gcagtgggta taatgatttta agttaaaagggt tttttttttt tttttttttt 3877
aacgtttttttt accttacccgttga aaaggagggtt caggaggggag acacaacata tttttttttt 3937
tggaaaaatgtt tttttttttt tttttttttt tttttttttt 3997
aacttcacgac ccaagttcat caatgttggaa taatatcagc tttaaataac aaaaaaatat 4057
ggactttaaa aaatctcaaa tttttttttt tttttttttt 4117

gtgcagcagt gcattcgccgg ctaactgcag cctcaagcac tggggctcaa gcaaaccctcc 4177
tgcctcagcc tcgtgagtag ctaggaccac aggtgcatgc caccatgcct ggctctaaag 4237
agaaaaaaaaa cttgatacca tagagccttg aatataaata tcctgatgtt aacctactgc 4297
tttgctgtg attttttttc cttagtgagt tttaaatctc aggcttagatt ttlathtt 4357
tttcgtgtg tglatgagac aaaataaaaaa taaatatatt tgccctgagt tt 4409

<210> 150

<211> 663

<212> PRT

<213> Homo sapiens

<400> 150

Met Ser Trp Leu Ser Ser Ser Gln Gly Val Val Leu Thr Ala Tyr His

1 5 10 15

Pro Ser Gly Lys Asp Gln Ala Val Gly Asn Ser His Ala Lys Ala Gly

20 25 30

Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln

35 40 45

Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe Asp Arg Ser

50 55 60

Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile

65 70 75 80

Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln

85 90 95

Glu Val Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu

100 105 110

Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly

115 120 125

Asp Pro Gln Glu Ser Ile Val Phe Leu Ser Thr Leu Thr Arg Thr Gln

130 135 140

Ala Ala Ala Val Gln Lys Arg Val Glu Thr Val Ser Gln Thr Leu Arg

145 150 155 160

Lys Lys Asn Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala

165 170 175

Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln

180 185 190

Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala

195 200 205

Ser Asn Leu Val Gly Glu Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro

210 215 220

Ala Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala

225 230 235 240

Leu Asn Gln Lys Glu Ser Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly

245 250 255

Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly

260 265 270

Thr Thr Arg Ile Gly Asp Leu Ala Pro Gln Asp Met Lys Lys Val Cys

275 280 285

His Leu Ala Leu Ile Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile

290 295 300

Glu Leu Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser Gly

305 310 315 320

Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys

325 330 335

Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg
340 345 350
Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly
355 360 365
Ala Ala Ile Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe
370 375 380
Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His Asp Ala Ala
385 390 395 400
Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser
405 410 415
Val Glu Tyr Leu Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys
420 425 430
Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp
435 440 445
Ala Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val
450 455 460
Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met
465 470 475 480
Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys Ser
485 490 495
Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met
500 505 510
His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe
515 520 525
Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His Lys Lys Asp
530 535 540
Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu

545 550 555 560
Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn Asp Ala Asp Val Pro Gln
565 570 575
Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
580 585 590
Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu Ala Arg Phe
595 600 605
Leu Ser Gln Glu Ser Gly Val Ala Gln Thr Leu Lys Lys Gly Glu Val
610 615 620
Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp
625 630 635 640
Asp Thr Tyr Met Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp
645 650 655
Val Ile Lys Ser Lys Pro Leu
660

<210> 151

<211> 4490

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)..(2591)

<400> 151

aa atg ggc tac atc ccc tcc tcc tat gtg cag ccc ttg aac tac cgg 47

Met Gly Tyr Ile Pro Ser Ser Tyr Val Gln Pro Leu Asn Tyr Arg

1 5 10 15

aac tca aca ctg agt gac agc ggt atg att gat aat ctt cca gac agc 95
Asn Ser Thr Leu Ser Asp Ser Gly Met Ile Asp Asn Leu Pro Asp Ser
20 25 30
cca gac gag gta gcc aag gag ctg gag ctg ctc ggg gga tgg aca gat 143
Pro Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp
35 40 45
gac aaa aaa gta cca ggc aga atg tac agt aat aac cct ttc tgg aat 191
Asp Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn
50 55 60
ggg gtc cag acc aat cca ttt ctg aat ggg aac gtg ccc gtc atg ccc 239
Gly Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro
65 70 75
agc ctg gat gag ctg aat ccc aaa agt act gtg gat ttg ctc ctt ttt 287
Ser Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Phe
80 85 90 95
gac gca ggt aca tcc tcc ttc acc gaa tcc agc tca gcc acc acg aat 335
Asp Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ala Thr Thr Asn
100 105 110
agc act ggc aac atc ttc gat gag ctt cca gtc aca aac ggg ctc cac 383
Ser Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His
115 120 125
gca gag ccg ccg gtc agg cgg gac aac ccc ttc ttc aga agc aag cgc 431
Ala Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg
130 135 140
tcc tac agt ctc tcg gaa ctc tcc gtc ctc caa gcc aag tcc gac gct 479
Ser Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala

145	150	155	
ccc aca tcg tcg agt ttc ttc acc ggc ttg aaa tca cct gcc ccc gag			527
Pro Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu			
160	165	170	175
caa ttt cag agc cggtt gag gat ttt cga act gcc tgg cta aac cac agg			575
Gln Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg			
180	185	190	
aag ctg gcc cggtt tct tgc cac gac ctg gac ttg ctt ggc caa agc cct			623
Lys Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro			
195	200	205	
gggtt tgg ggc cag acc caa gcc gtgtt gag aca aac atc gtgtt tgc aag ctg			671
Gly Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu			
210	215	220	
gat agc tcc ggg ggtt gct gtc cag ctt cct gac acc agc atc agc atc			719
Asp Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile			
225	230	235	
cac gtgtt ccc gag ggc cac gtc gcc cct ggg gag acc cag cag atc tcc			767
His Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser			
240	245	250	255
atg aaa gcc ctg ctg gac ccc ccgtt ctg gag ctc aac agt gac agg tcc			815
Met Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser			
260	265	270	
tgc agc atc agc cct gtgtt ctg gag gtc aag ctg agc aac ctg gag gtgtt			863
Cys Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val			
275	280	285	
aaa acc tct atc atc ttg gag atg aaa gtgtt tca gcc gag ata aaa aat			911
Lys Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn			

290	295	300	
gac ctt ttt agc aaa agc aca gtg ggc ctc cag tgc ctg agg agc gac 959			
Asp Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp			
305	310	315	
tcg aag gaa ggg cca tat gtc tcc gtc ccg ctc aac tgc agc tgt ggg 1007			
Ser Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly			
320	325	330	335
gac acg gtc cag gca cag ctg cac aac ctg gag ccc tgt atg tac gtg 1055			
Asp Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val			
340	345	350	
gct gtc gtg gcc cat ggc cca agc atc ctc tac cct tcc acc gtg tgg 1103			
Ala Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp			
355	360	365	
gac ttc atc aat aaa aaa gtc aca gtg ggt ctc tac ggc cct aaa cac 1151			
Asp Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His			
370	375	380	
atc cac cca tcc ttc aag acg gta gtg acc att ttt ggg cat gac tgt 1199			
Ile His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys			
385	390	395	
gcc cca aag acg ctc ctg gtc agc gag gtc aca cgc cag gca ccc aac 1247			
Ala Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn			
400	405	410	415
cct gcc ccg gtg gcc ctg cag ctg tgg ggg aag cac cag ttc gtt ttg 1295			
Pro Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu			
420	425	430	
tcc agg ccc cag gat ctc aag gtc tgt atg ttt tcc aat atg acg aat 1343			

Ser Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn
435 440 445
tac gag gtc aaa gcc agc gag cag gcc aaa gtg gtg cga gga ttc cag 1391
Tyr Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln
450 455 460
ctg aag ctg ggc aag gtg agc cgc ctg atc ttc ccc atc acc tcc cag 1439
Leu Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln
465 470 475
aac ccc aac gag ctc tct gac ttc acg ctg cgg gtt cag gtg aag gac 1487
Asn Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp
480 485 490 495
gac cag gag gcc atc ctc acc cag ttt tgt gtc cag act cct cag cca 1535
Asp Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro
500 505 510
ccc cct aaa agt gcc atc aag cct tcc ggg caa agg agg ttt ctc aag 1583
Pro Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys
515 520 525
aag aac gaa gtc ggg aaa atc atc ctg tcc ccg ttt gcc acc act aca 1631
Lys Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr
530 535 540
aag tac ccg act ttc cag gac cgc ccg gtg tcc agc ctc aag ttt ggt 1679
Lys Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly
545 550 555
aag ttg ctc aag act gtg gtg cgg cag aac aag aac cac tac ctg ctg 1727
Lys Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu
560 565 570 575
gag tac aag aag ggc gac ggg atc gcc ctg ctc agc gag gag cgg gtc 1775

Glu Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val
 580 585 590
 agg ctc cgg ggc cag ctg tgg acc aag gag tgg tac atc ggc tac tac 1823
 Arg Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr
 595 600 605
 cag ggc agg gtg ggc ctc gtg cac acc aag aac gtg ctg gtg gtc ggc 1871
 Gln Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly
 610 615 620
 agg gcc cgg ccc agc ctg tgc tcg ggc ccc gag ctg agc acc tcg gtg 1919
 Arg Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val
 625 630 635
 ctg ctg gag cag atc ctg cgg ccc tgc aaa ttc ctc acg tac atc tat 1967
 Leu Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr
 640 645 650 655
 gcc tcc gtg agg acc ctg ctc atg gag aac atc agc agc tgg cgc tcc 2015
 Ala Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser
 660 665 670
 ttc gct gac gcc ctg ggc tac gtg aac ctg ccg ctc acc ttt ttc tgc 2063
 Phe Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys
 675 680 685
 cgg gca gag ctg gat agt gag ccc gag cgg gtg gcg tcc gtc ctg gaa 2111
 Arg Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu
 690 695 700
 aag ctg aag gag gac tgt aac aac act gag aac aaa gaa cgg aag tcc 2159
 Lys Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser
 705 710 715

ttc cag aag gag ctt gtg atg gcc cta ctg aag atg gac tgc cag ggc 2207
Phe Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly
720 725 730 735
ctg gtg gtc aga ctc atc cag gac ttt gtg ctc ctg acc acg gct gta 2255
Leu Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val
740 745 750
gag gtg gcc cag cgc tgg cgga gatg ctg gct gag aag ctg gcc aag gtc 2303
Glu Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val
755 760 765
tcc aag cag cag atg gac gcc tac gag tct ccc cac cgg gac agg aac 2351
Ser Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn
770 775 780
ggg gtt gtg gac agc gag gcc atg tgg aag cct gcg tat gac ttc tta 2399
Gly Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu
785 790 795
ctc acc tgg agc cat cag atc ggg gac agc tac cgg gat gtc atc cag 2447
Leu Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln
800 805 810 815
gag ctg cac ctg ggc ctg gac aag atg aaa aac ccc atc acc aag cgc 2495
Glu Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg
820 825 830
tgg aag cac ctc act ggg act ctg atc ttg gtg aac tcc ctg gac gtt 2543
Trp Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val
835 840 845
ctg aga gca gcc gcc ttc agc cct gcg gac cag gac gac ttc gtg att 2591
Leu Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile
850 855 860

tgaatgggtc ccctccccc tcgtcgctc ggagtgcagg ccctttctg ccctgcgtc 2651
ccgtcgctca ccggggagct gaagaggggag gaaggggcgg ctgcgtcagac agatttaggg 2711
ccccccagct aggctacacc catcatgcgc cgcccttc ctcgaggaa gaggcctgaa 2771
gggactgcct actgcagctc gttgccaatc acatagctt ctatgtta agtataaatt 2831
taaatttaaa atcacaaaa taacgaatgg ggggaaggaa tctatgagaa aggtggtac 2891
taatttttt atggaccata aaggtttaaa agaaaatagg ggcacagggt gttgaggtt 2951
ttatgttgtt atagacctt ttaaatttalg tttagatgt atataggtat ttaaaggta 3011
ctgggagcat ttctgattcc cggccacact ttgcattca acactcagcc cggaaagatg 3071
ctcgltcggt tttggacct ctttcaactcc ctgcgtgtaa gaaggtaat cacgtggaa 3131
aaagtggctt ttcagtaaac gggtaacatc cattttttt gagaaggccc caggccctgc 3191
tccctcctcg gatttgatttgc tttccgtgc tttgcctcac tcgttagtaaa tgaccatcca 3251
tagaatalgt gaatctttgg tgagcttcag tggcagagt gaagtcccgc attagcattt 3311
aggtgccctg agctgttttgc cccaaatagat tagaaagcag ccatgagtttgc acagtcttta 3371
gggcccctgc cagttgtcaa ttagtcatgg acaagaacaa tgccatttga gagtgagggt 3431
gtccctgctg ctacgaggcc attgtactgt ttttcccttg aggtcaaagc agtgcttccc 3491
atagagtttgc tgccttc tttggacagg aagaaaactt catgaccgaa tcagagccctt 3551
ggtggccact gacttcgtc ttattgcag atgctgtgggt tggcctcaca agcaacgcct 3611
tatgctgtatg tgcagagggttgc ctagtgcctt tttgccttgc tttgcatttc atttcatcta 3671
aggcttaacc cctcttcctt cctgggtgtac ctgtgtctcc tcggaaaggaa gtcatagttt 3731
agatgaaacc attttttgttcaatgtaaatgatcatctgag caagatgagc attttgttaaa 3791
aatgaaaalgt tgactcacat aaaatcagga acttggcaca gtgtgcattt aataacttta 3851
gggtgcagac atgctgtgttgc aatctcacaa tgcgtcgtag atgicgcgtg ttggaaaggaa 3911
gcaggaggaa ggactgtatc tggcaatca gttaggttgc gtgtcccttgc gcaacgtgcc 3971
aggacacttc ctgtgtgcct gcagttgtca gggaccattt gggatcccga atctcatctt 4031
ctaaaactgc ttcttgaaa catgttactt ctttagtata atcaatgtat actcccttac 4091
tggcctgaaa cgttgatag ctacttattc agatactgaa gaccaacggaa ctgaaaaaaaa 4151

gaacaaacat tagctatittt atgctgcaag aaccaggaca cacaattcgc caatcatccc 4211
accatataac ctgcattgt gcttcataac tccacccat aatttctccc agagatcate 4271
tatcaccttt tccccaaaga agaaacaaaa ccagttgcac cttaaaccat ggalattttt 4331
tcctcagggg cttaaatag ttccatgc aacgtgtctt gtacacaaa taaaattcta 4391
caaaagtgc agtaaatttt attggatat tttaacctgt taagtgtgtg tgtgtttct 4451
gtacccaacc agacttaaa taaaacaaac atgaaacct 4490

<210> 152

<211> 863

<212> PRT

<213> Homo sapiens

<400> 152

Met Gly Tyr Ile Pro Ser Ser Tyr Val Gln Pro Leu Asn Tyr Arg Asn

1 5 10 15

Ser Thr Leu Ser Asp Ser Gly Met Ile Asp Asn Leu Pro Asp Ser Pro

20 25 30

Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp Asp

35 40 45

Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn Gly

50 55 60

Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro Ser

65 70 75 80

Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Phe Asp

85 90 95

Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ala Thr Thr Asn Ser

100 105 110

Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His Ala

115 120 125
Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg Ser
130 135 140
Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala Pro
145 150 155 160
Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu Gln
165 170 175
Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg Lys
180 185 190
Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro Gly
195 200 205
Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu Asp
210 215 220
Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile His
225 230 235 240
Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser Met
245 250 255
Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser Cys
260 265 270
Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val Lys
275 280 285
Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp
290 295 300
Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp Ser
305 310 315 320
Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly Asp
325 330 335

Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val Ala
340 345 350

Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp Asp
355 360 365

Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His Ile
370 375 380

His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys Ala
385 390 395 400

Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn Pro
405 410 415

Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu Ser
420 425 430

Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn Tyr
435 440 445

Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln Leu
450 455 460

Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln Asn
465 470 475 480

Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp Asp
485 490 495

Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro Pro
500 505 510

Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys
515 520 525

Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys
530 535 540

Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys
545 550 555 560
Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu Glu
565 570 575
Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val Arg
580 585 590
Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr Gln
595 600 605
Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly Arg
610 615 620
Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val Leu
625 630 635 640
Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr Ala
645 650 655
Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser Phe
660 665 670
Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys Arg
675 680 685
Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu Lys
690 695 700
Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser Phe
705 710 715 720
Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly Leu
725 730 735
Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val Glu
740 745 750
Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val Ser

755 760 765
Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn Gly
770 775 780
Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu Leu
785 790 795 800
Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln Glu
805 810 815
Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg Trp
820 825 830
Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val Leu
835 840 845
Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile
850 855 860

<210> 153

<211> 2194

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133)..(1125)

<400> 153

ggtgccgcgc tggccccctc agagggttcc tgctgctgcc ggtgccttgg accctcccccc 60
tcgccttcgc ttctactgcc ccaggagccc ggcgggtccg ggactccgt ccgtgccggt 120
gcgggcgcgc gc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc cct 171

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro

1

5

10

ttc tcc ttc ctg ctg cta gtg ctg ctg gtg acg cgg agc ccg gtc 219
Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val
15 20 25
aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc ttc 267
Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe
30 35 40 45
agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag ccc 315
Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro
50 55 60
cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac gcg 363
Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala
65 70 75
ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga gca 411
Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala
80 85 90
aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct gtc 459
Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val
95 100 105
tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg cga 507
Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg
110 115 120 125
ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca gca 555
Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala
130 135 140
aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc cta 603
Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu

145	150	155	
agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc ttt			651
Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe			
160	165	170	
gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa atg			699
Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met			
175	180	185	
tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct ttc			747
Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe			
190	195	200	205
ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta ata			795
Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile			
210	215	220	
aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat ggg			843
Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly			
225	230	235	
aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg atg			891
Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met			
240	245	250	
gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg tgt			939
Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys			
255	260	265	
gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc tac			987
Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr			
270	275	280	285
ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act gtt			1035
Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val			

290	295	300	
aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc agc			1083
Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser			
305	310	315	
tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc			1125
Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe			
320	325	330	
tagacttca cggtgggacg aaacgggttc agaaaactgcc aggggcctca tacagggata			1185
tcaaaatacc ctgttgctca gcccaggccc tggggaatca ggtgactcac acaaatgcaa			1245
tagtttgtca ctgcattttt acctgaacca aagctaaacc cggtgttgcc accatgcacc			1305
atggcatgcc agagtcaac actgttgctc ttgaaaatct gggctgaaa aaacgcacaa			1365
gagccccctgc cctgccttag ctgaggcaca cagggagacc cagtgaggat aagcacagat			1425
tgaattgtac agtttgaga tgcagatgt aatgcattgg acatgcata taactcagag			1485
ttgacatttt aaaacttgcc acacttattt caaatatttg tactcagcta tgtaaacatg			1545
tactgttagac atcaaacttg tggccatact aataaaatta ttaaaaggag cactaaagga			1605
aaactgtgtg ccaagcatca tatictaagg catacgaat ttggggaaagc caccatgcaa			1665
tccagtgagg cttagtgtc cagcaaccaa aatggtaggg aggtcttcaa gccaatgagg			1725
gatttatagc atcttgcata gagagctgca aaccaccagg gggcagagtt gcattttcc			1785
aggctttta ggaagctctg caacagatgt gatctgatca taggcaatta gaactggaag			1845
aaacttccaa aaatatctgt gtgtgcctc attttacaaa tgaggaaact aaactctgt			1905
gaagggaaagg ggttgcctca aaagtcacag cttagctggg cacagtggct catgccata			1965
atcccagcaa ttcaaaaaac tgaggcagga ggattacgtt agggcagact gggcaatata			2025
gcaagacccc atctctaaaa aataggcat ggtggtgcat gcctgtattc ccagctactc			2085
aggaggttga ggtgggagga tcacttgagc ccagaagttc aaggctgcaa tgagccatga			2145
ttacaccacg gcactacaac ctggggca cagtgagaac ctgacttt			2194

<211> 331

<212> PRT

<213> Homo sapiens

<400> 154

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe

1 5 10 15

Leu Leu Leu Val Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys

20 25 30

Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu

35 40 45

Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg

50 55 60

Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn

65 70 75 80

Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val

85 90 95

Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His

100 105 110

Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp

115 120 125

Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg

130 135 140

Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala

145 150 155 160

Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys

165 170 175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu

180 185 190

Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu

195 200 205

Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

210 215 220

Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg

225 230 235 240

Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu

245 250 255

Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser

260 265 270

Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys

275 280 285

Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe

290 295 300

Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr

305 310 315 320

Asp Ser Met Val Glu Asp Cys Glu Pro His Phe

325 330

<210> 155

<211> 3377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44)..(1666)

<400> 155

gcctctgcac ccctactgct tctgcgttga aggccggaggc tcc atg ttg tcc cct 55

Met Leu Ser Pro

1

cag cga gtg gga gca gct gcc tca aga gga gca gat gat gcc atg gag 103

Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp Asp Ala Met Glu

5

10

15

20

agc agc aag cct ggt cca gtg cag gtt ttg gtt cag aaa gat caa 151

Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val Gln Lys Asp Gln

25

30

35

cat tcc ttt gag cta gat gag aaa gcc ttg gcc agc atc ctc ttg cag 199

His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser Ile Leu Leu Gln

40

45

50

gac cac atc cga gat ctt gat gtg gtg gtg gtt tca gtg gct ggt gcc 247

Asp His Ile Arg Asp Leu Asp Val Val Val Ser Val Ala Gly Ala

55

60

65

ttc cga aag ggc aag tcc ttc att ctg gat ttt atg cta cga tac tta 295

Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met Leu Arg Tyr Leu

70

75

80

tat tct cag aag gaa agt ggc cat tca aat tgg ttg ggt gac cca gaa 343

Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu Gly Asp Pro Glu

85

90

95

100

gaa ccg tta aca gga ttt tcc tgg aga ggg gga tct gat cca gaa acc 391

Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser Asp Pro Glu Thr

105

110

115

act ggg att caa atc tgg agt gaa gtt ttc act gtg gag aag cca ggt 439

Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val Glu Lys Pro Gly
 120 125 130
 ggg aag aag gtt gca gtt gtt ctg atg gat acc cag ggg gca ttt gac 487
 Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln Gly Ala Phe Asp
 135 140 145
 agc cag tca act gtg aaa gac tgt gct acc alc ttt gct cta agc act 535
 Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe Ala Leu Ser Thr
 150 155 160
 atg act agt tct gtt cag att tat aat tta tct cag aac att caa gaa 583
 Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln Asn Ile Gln Glu
 165 170 175 180
 gat gat ctt caa cag ctg cag ctc ttc aca gaa tac ggt cgt ctg gca 631
 Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr Gly Arg Leu Ala
 185 190 195
 atg gat gaa att ttc caa aag cct ttc cag aca ctg atg ttt ttg gtt 679
 Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu Met Phe Leu Val
 200 205 210
 aga gat tgg agt ttc cct tat gaa tat agc tat gga ctc caa gga gga 727
 Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly Leu Gln Gly Gly
 215 220 225
 atg gca ttt ttg gat aag cgt tta cag gtg aag gaa cat caa cat gaa 775
 Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu His Gln His Glu
 230 235 240
 gaa att cag aat gtt cga aat cac att cac tca tgt ttc tcc gat gtc 823
 Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys Phe Ser Asp Val
 245 250 255 260

acc tgc ttt ctc tta cca cat cca gga ctc cag gtg gcc aca agc cct 871
 Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val Ala Thr Ser Pro
 265 270 275
 gac ttt gat ggg aaa tta aaa gat att gct ggt gaa ttc aaa gag cag 919
 Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu Phe Lys Glu Gln
 280 285 290
 tta cag gca ctg ata ccg tat gta tta aac cca tct aag tta atg gaa 967
 Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser Lys Leu Met Glu
 295 300 305
 aag gag atc aat ggc tca aag gtc acc tgt cgg gga cta ctg gag tat 1015
 Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly Leu Leu Glu Tyr
 310 315 320
 ttt aag gca tat att aaa att tat caa gga gaa gat ctg cct cac ccc 1063
 Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp Leu Pro His Pro
 325 330 335 340
 aag tcc atg ctt cag gcc act gct gaa gcc aac aac tta gca gct gca 1111
 Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Ala
 345 350 355
 gcc tct gcc aag gac att tat tat aac aac atg gaa gag gtt tgt ggg 1159
 Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu Glu Val Cys Gly
 360 365 370
 gga gag aaa cct tat ttg tct cca gac att cta gag gag aag cac tgt 1207
 Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu Glu Lys His Cys
 375 380 385
 gaa ttc aaa caa ctt gct ctg gac cat ttt aag aag acc aag aag atg 1255
 Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys Thr Lys Lys Met
 390 395 400

ggt ggg aag gat ttc agc ttt cgt tac cag cag gag ctg gag gag gaa 1303
 Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu Leu Glu Glu Glu
 405 410 415 420
 atc aag gaa tta tat gag aac ttc tgc aag cac aat ggt agc aag aac 1351
 Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn Gly Ser Lys Asn
 425 430 435
 gtc ttc agc acc ttc cga acc cct gca gtg ctg ttc acg ggc att gta 1399
 Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe Thr Gly Ile Val
 440 445 450
 gct ttg tac ata gcc tca ggc ctc act ggc ttc ata ggt ctt gag gtt 1447
 Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile Gly Leu Glu Val
 455 460 465
 gta gcc cag ttg ttc aac tgt atg gtt gga cta ctg tta ata gca ctc 1495
 Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu Ile Ala Leu
 470 475 480
 ctc acc tgg ggc tac atc agg tat tct ggt caa tat cgt gag ctg ggc 1543
 Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr Arg Glu Leu Gly
 485 490 495 500
 gga gct att gat ttt ggt gcc gca tat gtg ttg gag cag gct tct tct 1591
 Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu Gln Ala Ser Ser
 505 510 515
 cat atc ggt aat tcc act cag gcc act gtg agg gat gca gtt gtt gga 1639
 His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp Ala Val Val Gly
 520 525 530
 -aga cca tcc atg gat aaa aaa gct caa tagcatctt acgtgaagat 1686
 Arg Pro Ser Met Asp Lys Lys Ala Gln

535

540

caaacaagaa cacaacaagc ccctactgat ttctgggtt ctgccacggc cacaggttca 1746
tatccagagg aatggcagat ctgagacgat ccaggaagag ctaaaacatg gccctgtaat 1806
aatgagcag accttcctg tggttcaaa ttaattaaaca cacttcatt tcttttgaa 1866
gcatttttt tccttgctgt tatagatgca agcctgtgtc tattttata ttactctgtc 1926
tttgtgcactt tatggaggag gaagcttagag gaaaaatgga aatgcagctt ttaagttttt 1986
tatgtgccac ttagtgcctt ttaagaltga ttccatggt tgcacacac gatggggagg 2046
ggatggagga taacctcatg aaaggigcca ttttcgggtg aaacttgaca tttttttat 2106
actttacttt tgagaaggat tcttttttt ttagtttgaa gtctcgctt gtccaccaggc 2166
ttgagtgca ggtgtgtatc ttggctcaact gcaacctctg cctgcccgggt tcaaggcattt 2226
ctcctgcctc agcccccua gtagctggga ctacagggt acgccaccat acccagctaa 2286
ttttttgtt ttttttagtag agatggggtt tcaccatgtt ggccaggatg gtctttggct 2346
cttgaccctt gatccgcctt gcccgcctt gcctcccaa gtgtggat tacaggcgtt 2406
agccaccgtt cccggccaag aaggatttctt ttttaaaag tttacagaac ttggagaaac 2466
ttcagaacta aagactaact gaaaatgtt tcattacact caaaaaaaaaat ttacaatagg 2526
gaatcctgtt gccacatagt gtggaaaaat catgtcatat ttaatatac catacttga 2586
aatgtgaggt ttttacccag taggctgaca gtttttttgc aacttgcctt atttttttt 2646
ttttttggtc cctatacgctt ctttctagaa aaaggaggcaa acgtgcctt gaaagccaga 2706
gtggctcata ataaaaggaa tgcgttagat acttcaagaa aaaagctaag tttaaatgaa 2766
ccatgtgacc tctgataagt cacttgaact tglgccttag tcaggttcac tgltaggttta 2826
catatgtatg tatgttttac acaactctt gtaattgtcat ttgaggggtt cacttcctcc 2886
tcccccccccc tgggagcggc cctgcgtgt cactgacatc tcattaaaaaa aaaaaaaaaa 2946
tttgctctca aggtgtttga ggctttaaatg caacccttta gcccttgggtt ctttttgggt 3006
caagaattct ggctgtttac ctcagactca gaccctgaa atgttgcctaa attcttcaaa 3066
taactgtttt gggggggggg ggagatgaaa gagagtgcgc ttttttttac agttaaagac 3126
atccaatatc ttaaaaagga gttttccctt agaaacacac acacccttcc tcttgcctaa 3186
aagatctcac tccatgatac tggtaaaat atttttgcac tgggtgaag ttttttgac 3246

tttttctgt acataactgt gttctcagag ctgaatgtt atatctttg ctgtgcaaaa 3306
gaaacatgta aaatgttgtt cagttgtata tacagaaatg tgtataaaac atttgttat 3366
ttttaaaag t 3377

<210> 156

<211> 541

<212> PRT

<213> Homo sapiens

<400> 156

Met Leu Ser Pro Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp

1 5 10 15

Asp Ala Met Glu Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val

20 25 30

Gln Lys Asp Gln His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser

35 40 45

Ile Leu Leu Gln Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser

50 55 60

Val Ala Gly Ala Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met

65 70 75 80

Leu Arg Tyr Leu Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu

85 90 95

Gly Asp Pro Glu Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser

100 105 110

Asp Pro Glu Thr Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val

115 120 125

Glu Lys Pro Gly Gly Lys Val Ala Val Val Leu Met Asp Thr Gln

130 135 140

Gly Ala Phe Asp Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe
145 150 155 160
Ala Leu Ser Thr Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln
165 170 175
Asn Ile Gln Glu Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr
180 185 190
Gly Arg Leu Ala Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu
195 200 205
Met Phe Leu Val Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly
210 215 220
Leu Gln Gly Gly Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu
225 230 235 240
His Gln His Glu Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys
245 250 255
Phe Ser Asp Val Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val
260 265 270
Ala Thr Ser Pro Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu
275 280 285
Phe Lys Glu Gln Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser
290 295 300
Lys Leu Met Glu Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly
305 310 315 320
Leu Leu Glu Tyr Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp
325 330 335
Leu Pro His Pro Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn
340 345 350

Leu Ala Ala Ala Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu

355 360 365

Glu Val Cys Gly Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu

370 375 380

Glu Lys His Cys Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys

385 390 395 400

Thr Lys Lys Met Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu

405 410 415

Leu Glu Glu Glu Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn

420 425 430

Gly Ser Lys Asn Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe

435 440 445

Thr Gly Ile Val Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile

450 455 460

Gly Leu Glu Val Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu

465 470 475 480

Leu Ile Ala Leu Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr

485 490 495

Arg Glu Leu Gly Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu

500 505 510

Gln Ala Ser Ser His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp

515 520 525

Ala Val Val Gly Arg Pro Ser Met Asp Lys Lys Ala Gln

530 535 540

<210> 157

<211> 2172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45)..(563)

<400> 157

ggaacacggc acccgactg cgctcatgg tgcaggctg gtat atg gac gac gcc 56

Met Asp Asp Ala

1

ccg ggc gac ccg cgg caa ccc cac cgc ccc gac ccc ggc cgc cca gtg 104

Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro Gly Arg Pro Val

5 10 15 20

ggc ctg gag cag ctg cgg cgg ctc ggg gtg ctc tac tgg aag ctg gat 152

Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp

25 30 35

gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga aga gag 200

Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu

40 45 50

agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat aaa cta 248

Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu

55 60 65

cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat ttg cac 296

Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His Leu His

70 75 80

ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac ttc gat 344

Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp

85 90 95 100

gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag aag gga 392
 Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu Lys Gly
 105 110 115

 gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg gtg gac 440
 Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp
 120 125 130

 gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa ccg gtg 488
 Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val
 135 140 145

 tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc ggg cag 536
 Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln
 150 155 160

 tac gtg aaa ttt ctg gca cag acc gcc tagcagtgt gcctggaaac 583
 Tyr Val Lys Phe Leu Ala Gln Thr Ala
 165 170

 taacacgtgc ctcgtaaagg tccccatgt aatgactgag cagaaaatca atcacttct 643
 ctttgccttt agaggatagc cttgaggcta gattatcttt cttttaag attatttgat 703
 cagaatattt tgtaatgaaa ggatctagaa agcaacttgg aagtgtaaag agtcaccc 763
 atttctgtt actcaatcaa gactggtggg tccatggccc tgttgttagtt catgcattca 823
 gttgagtccc aaatgaaagt ttcatctccc gaaatgcagt tccttagatg cccatctgga 883
 cgtgatgccc cgcctgccgt gtaagaaggt gcaatccatg alaacacagc tagccagata 943
 gaagacactt tttctccaa aatgatgcct tgggtgggg aglgttaggg ggaagagctc 1003
 ccaccctaag gggcacacac tgagttgcct atgccacttc ctgtttcaaa ataaagtaac 1063
 tgccttaatc ttatactcat ggcttggagt taccttatat tcaggtatat gtgatattt 1123
 gcctggtttg ttaaaattgc cccatttaga ttccttctat aattgttctt atagataagt 1183
 aatttatata tgagctgtgt tagtatttt tcagtgtgag atctctggat tctttcacaa 1243

taaagctttttaac aggagttatata gtacataaat ttctactca acaattccga 1303
 gataggatta tgcccttagttt gtcataatcac agaaaaactc caagttaact tcatttttg 1363
 gaagggcagg tcgttttaa agtattttttt ttttaactg gatgaaaaat ctcatgtta 1423
 ggattttttt tcttaatcac ctccacactg tacagaggaa actcaaggct taaatgtttt 1483
 agttaaactct gtcctcagttt taggattaaa ataccacccg gtgggtgtat gatgccatat 1543
 accgcaggc ttgcctctgtt caagttgtac tctatctcg taattttttt aagtgcgtat 1603
 ctactgattt ttttaatgg attcatttttctt aaatggcat tataaataga gcttgttcat 1663
 ttttaagaac gaaacattca tatgataaaac tatcgctttt aattgcctttt cttgcttcat 1723
 ataacttttc cctgtcagga tccttagtgtt ttgaaactcc tcgtgcgggg ctggccctt 1783
 gcggactcta gtttcgcctc cttgtatgtgg cgccctggat ttcttcaattt cagagctgtt 1843
 tttttacagg caagagtaag ttcctggca cagtggctca tgcctgttaat cttagctact 1903
 caggaggcttta aggtggggagg attcttagag cctgggaggtt cgaggctgca gtgagctgt 1963
 attgtggcca ctgcactcca gcctgggtga cagagcgaga ctctgtctca aaaaagaaga 2023
 aagagtaaga gctgaggcat ataaiagaat tctgctaaag cacttaaggtt gaaatcacat 2083
 tttctttcc caggatgttg ctacatctt tcgtttttat tgaggtgtca tttatgtaca 2143
 ataaaatgttta ctcattttca gtgtttttt 2172

<210> 158

<211> 173

<212> PRT

<213> Homo sapiens

<400> 158

Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro

1	5	10	15
---	---	----	----

Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr

20	25	30
----	----	----

Trp Lys Leu Asp Ala Asp Tyr Glu Asn Asp Pro Glu Leu Glu Lys

35 40 45
Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys

50 55 60
Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu

65 70 75 80
Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser

85 90 95
Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe

100 105 110
Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg

115 120 125
Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val

130 135 140
Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu

145 150 155 160
Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala

165 170

<210> 159

<211> 20

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 159

ggaagtgtta cttctgtctc 20

<210> 160

<211> 50

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 160

gagagagaga gagagagaga actagtctcg agttttttt tttttttttt 50

<210> 161

<211> 41

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 161

gagagagaga gagagagcgg ccgcactagt cccccccccc c 41

<210> 162

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo-cap linker sequence

<400> 162

agcaucgagu cggccuuguu ggccuacugg 30

<210> 163

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo(dT) primer sequence

<400> 163

gcggctgaag acggcctatg tggccttttt tttttttttt tt 42

<210> 164
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer sequence
 <400> 164
 agcatcgagt cggccttgtt g 21

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer sequence
 <400> 165
 gcggctgaag acggccatag t 21

<210> 166
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer sequence
 <400> 166
 actttattgt catagtttag atctatttg 30

<210> 167
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer sequence
 <400> 167
 ataatcctta aaaactccat ttccacccct 30

<210> 168
 <211> 1536
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (139).. (1062)
 <400> 168
 GTGCTCCGCC GCCCGCCCCG ACCCGGGCCC AGCCGCCTCC ACGGCCCGCG CTCGTACTGG 60
 AGCGAAGAGC GGCCTCCTGA GGGAGGGGAA GGGACGTGGG GGCGGCCACG GCAGGGATTAA 120
 CCTCCATTTC AGCTAACATG GGA GAG ATT AAA GTC TCT CCT GAT TAT AAC 171
 Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn
 1 5 10

TGG TTT AGA GGT ACA GTT CCC CTT AAA AAG ATT ATT GTG GAT GAT GAT			219
Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp	15	20	25
GAC AGT AAG ATA TGG TCG CTC TAT GAC GCG GGC CCC CGA AGT ATC AGG			267
Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg	30	35	40
TGT CCT CTC ATA TTC CTG CCC CCT GTC AGT GGA ACT GCA GAT GTC TTT			315
Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe	45	50	55
TTC CCG CAG ATT TTG GCT CTG ACT GGA TGG GGT TAC CGG GTT ATC GCT			363
Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala	60	65	70
60	65	70	75
TTG CAG TAT CCA GTT TAT TGG GAC CAT CTC GAG TTC TGT GAT GGA TTC			411
Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe	80	85	90
80	85	90	
AGA AAA CTT TTA GAC CAT TTA CAA TTG GAT AAA GTT CAT CTT TTT GGC			459
Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His Leu Phe Gly	95	100	105
95	100	105	
GCT TCT TTG GGA GGC TTT TTG GCC CAG AAA TTT GCT GAA TAT ACT CAC			507
Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His	110	115	120
110	115	120	
AAA TCT CCT AGA GTC CAT TCC CTA ATC CTC TGC AAT TCC TTC AGT GAC			555
Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp	125	130	135
125	130	135	
ACC TCT ATC TTC AAC CAA ACT TGG ACT GCA AAC AGC TTT TGG CTG ATG			603
Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met	140	145	150
140	145	150	155
CCT GCA TTT ATG CTC AAA AAA ATA GTT CTT GGA AAT TTT TCA TCT GGC			651
Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly	160	165	170
160	165	170	
CCG GTG GAC CCT ATG ATG GCT GAT GCC ATT GAT TTC ATG GTA GAC AGG			699
Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg	175	180	185
175	180	185	
CTA GAA AGT TTG GGT CAG AGT GAA CTG CCT TCA AGA CTT ACC TTG AAT			747
Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn	190	195	200
190	195	200	
TGT CAA AAT TCT TAT GTG GTA CCT CAT AAA ATT CGG GAC ATA CCT GTA			795
Cys Gln Asn Ser Tyr Val Val Pro His Lys Ile Arg Asp Ile Pro Val	205	210	215
205	210	215	

ACT ATT ATG GAT GTG TTT GAT CAG AGT GCG CTT TCA ACT GAA GCT AAA Thr Ile Met Asp Val Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys 220 225 230 235	843
GAA GAA ATG TAC AAG CTG TAT CCT AAT GCC CGA AGA GCT CAT CTG AAA Glu Glu Met Tyr Lys Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys 240 245 250	891
ACA GGA GGC AAT TTC CCA TAC CTG TGC AGA AGT GCA GAG GTC AAT CTT Thr Gly Gly Asn Phe Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu 255 260 265	939
TAT GTA CAG ATA CAT TTG CTG CAA TTC CAT GGA ACC AAA TAC GCG GCC Tyr Val Gln Ile His Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala 270 275 280	987
ATT GAC CCA TCA ATG GTC AGT GCC GAG GAG CTT GAG GTG CAG AAA GGC Ile Asp Pro Ser Met Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly 285 290 295	1035
AGC CTT GGC ATC AGC CAG GAG GAG CAG TAGTGTGTCT CTCGCTGTCA ATGATGA Ser Leu Gly Ile Ser Gln Glu Glu Gln 300 305	1089
GTTGACCCGG TGTGTTCTTG TATAGTCAGT GGCACTCAGCA CCCGTCAGCC GGCCCTTTCC TTCAGGTTCG TCAGGCTCAC CGGTTCTCAC TGTGTCTGGG AAGTAGGACT GATGGTCATC TTCATGACAG GCGGCATCTC CACTAAGCCT GTGTAACGT TCCCTCTTG GTTTCTTAG CTTTGAATT TGAAGAAGTA CTTTGAAAGA CTCCCATTAA AAGAACCGTG CAGATTTGC TACCAAAAGT CTTCACCACT GTGTTCTTAA GTGAATGTTA ATTCTGAGG TTTGGGACTT TGTGGTGGTT TTTTCTTCT TTTCTTTCC ATTCTTCTT CTTCTTTTT ATGTTGTTG CTGTAAATGC TGCACATCCA GATTGCATAT CAGGACATTG GTTATTTAT GCTTCTTGG ATATAACCAT GATCAGAGTG CCATGGC	1149 1209 1269 1329 1389 1449 1509 1536
<210> 169 <211> 308 <212> PRT <213> Homo sapiens <400> 169	
Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr 1 5 10 15	
Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Asp Ser Lys Ile Trp 20 25 30	
Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe 35 40 45	
Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu 50 55 60	
Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val 65 70 75 80	
Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp 85 90 95	
His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly 100 105 110	
Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val	

115	120	125
His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn		
130	135	140
Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu		
145	150	155
Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met		
165	170	175
Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly		
180	185	190
Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn Cys Gln Asn Ser Tyr		
195	200	205
Val Val Pro His Lys Ile Arg Asp Ile Pro Val Thr Ile Met Asp Val		
210	215	220
Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys Glu Glu Met Tyr Lys		
225	230	235
Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys Thr Gly Gly Asn Phe		
245	250	255
Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu Tyr Val Gln Ile His		
260	265	270
Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala Ile Asp Pro Ser Met		
275	280	285
Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly Ser Leu Gly Ile Ser		
290	295	300
Gln Glu Glu Gln		
305		

<210> 170

<211> 2560

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

(202)..(1002)

<400> 170

CTGGCCTACT GGGGCTCCAG CCGTGTCTTG AGGAGCTGGA CCAGCCACAT CCCCTGGGGC	60	
TGCAGTTGAA GCAGAACCAA GTGGCCATCC CGGCCTTAGA CCGTAGGTTC CTGGTCCCGG	120	
AGTGGTCGGA GCCCCGCCAGT GGGCAGGCAG CTCTGCTCA CAGGCCGCGG TGCCCAGGCC	180	
GCTGGCTCTC CGCAGGGCGG A ATG GCG CTG CAA GTG GAG CTG GTA CCC ACC	231	
Met Ala Leu Gln Val Glu Leu Val Pro Thr		
1	5	10

GGG GAG ATC ATC CGC GTG GTT CAT CCC CAC AGG CCC TGC AAG CTT GCC	279	
Gly Glu Ile Ile Arg Val Val His Pro His Arg Pro Cys Lys Leu Ala		
15	20	25

CTG GGC ACT GAC GGG GTT CGG GTG ACC ATG GAG AGT GCG CTC ACC GCC	327	
Leu Gly Ser Asp Gly Val Arg Val Thr Met Glu Ser Ala Leu Thr Ala		
30	35	40

CGT GAC CGG GTG GGG GTG CAG GAT TTC GTG CTG CTG GAG AAC TTC ACC	375	
Arg Asp Arg Val Gly Val Gln Asp Phe Val Leu Leu Glu Asn Phe Thr		
45	50	55

AGC GAG GCC CCC TTC ATC GGG AAC CTG CGG CGG CGA TTT CGG GAG AAT Ser Glu Ala Ala Phe Ile Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn	60	65	70	423
CTC ATC TAC ACC TAC ATT GGC CCC GTC CTG GTC TCT GTC AAT CCC TAC Leu Ile Tyr Thr Tyr Ile Gly Pro Val Leu Val Ser Val Asn Pro Tyr	75	80	85	90
CGG GAC CTG CAG ATC TAC AGC CGG CAG CAT ATG GAG CGT TAC CGT GGC Arg Asp Leu Gln Ile Tyr Ser Arg Gln His Met Glu Arg Tyr Arg Gly	95	100	105	519
GTC AGC TTC TAT GAA GTG CCC CCT CAC CTG TTT GCC GTG GCG GAC ACT Val Ser Phe Tyr Glu Val Pro His Leu Phe Ala Val Ala Asp Thr	110	115	120	567
GTG TAC CGA GCA CTG CGC ACG GAG CGT CGG GAC CAG GCT GTG ATG ATC Val Tyr Arg Ala Leu Arg Thr Glu Arg Arg Asp Gln Ala Val Met Ile	125	130	135	615
TCT GGG GAG AGC GGG GCA GGC AAG ACC GAG GCC ACC AAG AGG CTG CTG Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu	140	145	150	663
CAG TTC TAT GCA GAG ACC TGC CCA GCC CCC GAG CGC GGA GGT GCC GTG Gln Phe Tyr Ala Glu Thr Cys Pro Ala Pro Glu Arg Gly Gly Ala Val	155	160	165	711
CGG GAC CGG CTG CTA CAG AGC AAC CCG GTG CTG GAG GCC TTT GGA AAT Arg Asp Arg Leu Leu Gln Ser Asn Pro Val Leu Glu Ala Phe Gly Asn	175	180	185	759
GCC AAG ACC CTC CGG AAC GAT AAC TCC AGC AGG TTC GGG AAG TAC ATG Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met	190	195	200	807
GAT GTG CAG TTT GAC TTC AAG GGT GCC CCC GTG GGT GGC CAC ATC CTC Asp Val Gln Phe Asp Phe Lys Gly Ala Pro Val Gly Gly His Ile Leu	205	210	215	855
AGT TAC CCC CTG GAA AAG TCA CGA GTG GTG CAC CAG AAT CAT GGG GAG Ser Tyr Pro Leu Glu Lys Ser Arg Val Val His Gln Asn His Gly Glu	220	225	230	903
CGG AAC TTC ACA TCT ACC AGC TGC TGG AGG GGG GCG AGG AGG AGA Arg Asn Phe Thr Ser Ser Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg	235	240	245	951
CTC TTC GCA GGC TGG GCT TGG AAC GGA ACC CCC AGA GCT ATC TGT ACC Leu Phe Ala Gly Trp Ala Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr	255	260	265	999
TGG TGAAGGCCAG TGTGCCAAAG TCTTCTTCAT CAACGACAAG AGTGACTGGA AGGTCTG				1058

Trp

TCAGGAAGGC	TCTGACAGTC	ATTGATTCA	CCGAGGATGA	AGTGGAGGAC	CTGCTGAGCA	1118
TCGTGGCCAG	CGTCCTTCAT	TTGGGCAACA	TCCACTTGC	TGCCAACGAG	GAGAGCAATG	1178
CCCAGGTCAC	CACCGAGAAC	CAGCTCAAGT	ATCTGAGCCC	ATTCACTATG	CGGTGCCTGT	1238
TGTGAAATAC	GACCGCAAGG	GCTACAAGCC	TCGCTCCGG	CAGCTGCTGC	TCACGCCAA	1298
CGCCGTCGTC	ATCGTGGAGG	ACGCCAAAGT	CAAGCAGAGG	ATTGATTACG	CCAACCTGAC	1358
CGGAATCTCT	GTCAGCAGCC	TGAGCGACAG	TCTTTTGTG	CTTCATGTAC	AGCGTGCGGA	1418
CAATAAGCAA	AAGGGAGATG	TGGTGCTGCA	GAGTGACCAC	GTGATTGAGA	CGCTGACCAA	1478
GACAGCCCTC	AGTGCCAACC	GGGTGAACAG	CATCAACATC	AACCAGGGCA	GCATCACGTT	1538
TGCAGGGGGC	CCCGCAGGG	ATGGCACCAT	TGACTTCACA	CCCGGCTCGG	AGCTGCTCAT	1598
CACCAAGGCC	AAGAACGGGC	ACCTGGCTGT	GGTCGCCCCA	CGGCTGAATT	CTCGGTGATA	1658
AAGGCGCCCA	CTGGACCCCTC	CCAACGCCCA	ATGCTTGCT	TTTCTCCTCC	TCCCCTTCCC	1718
AGTTACCAAA	GACTCGAACT	TCCAGACAGG	GACCCAGGGA	CACCCCGAAG	CCCACCTGCA	1778
ATCTCCCACC	TCCTGCCAT	CCCTCTCTTG	AGGGAGCAGC	AGGGGCCAGG	AGCTACCCCA	1838
GGAGTGGGCC	AGGCCGGGCC	ACAGCAATAG	GAAAGCCAGG	GCCAGAGCGA	GCCATGCCAG	1898
CCCTACTGCCC	GATGCCAAAT	ATTGAGAGA	AGGGAACATT	TGCTGAGGTT	TTCTCTGAGG	1958
TTTTTTTGTA	TGCTTTATAG	GAAACTATT	TTTAAAAAAA	GCCATTCCC	ACCCAAGGAC	2018
ACAGTGGATG	TGTTTCCCT	GACTCCAGCA	GGGCAAGGAA	ATGTAGCCGA	GAGGTTGTGT	2078
GGGCTGGGCT	CTGGTGCCT	CTTCCCTGGC	CAGGACACCT	CTCCTCCTGA	TCCCCTTGGC	2138
ACCTTGCTCT	TCTGTCTGTT	TACCTGTCTC	CCTGCCTGCC	CATCTGCATC	TTTTGCAGCC	2198
CACTCTGACT	TCCATCTGGG	GGCTGAGACC	ACCCCTGCC	GCCCCCTTCT	TTCTGCCTTA	2258
AGAATGTCTT	TTTAGGCTGG	GCATGGTGGC	TCACGCCGT	AACCCAGCA	CTTGGGAGG	2318
CGGAGACGGG	CAGATAACCT	GAGGTCAAGGA	TTTCGAGACC	AACCTGACCT	ACATGGAGAA	2378
ACTCCGCCTC	TGGTAAGGAT	ACAAAATTAG	CCGGGCATGG	TGGTGCACGC	CTCTAATCCC	2438
AGCTGCTCGG	GAGGCTGAGG	CAGGAGAAC	ACTTGAACCC	GGGAAGTGG	GGTTGCAGTG	2498
AGCCAAGAGT	ACACCACTGC	ACTCCAGCCT	GGGCAACAGA	GCGAGACTCC	GTCTAAAAA	2558
AA						2560

<210> 171

<211> 267

<212> PRT

<213> Homo sapiens

<400> 171

Met	Ala	Leu	Gln	Val	Glu	Leu	Val	Pro	Thr	Gly	Glu	Ile	Ile	Arg	Val
1				5				10				15			
Val	His	Pro	His	Arg	Pro	Cys	Lys	Leu	Ala	Leu	Gly	Ser	Asp	Gly	Val
							20			25			30		
Arg	Val	Thr	Met	Glu	Ser	Ala	Leu	Thr	Ala	Arg	Asp	Arg	Val	Gly	Val
			35				40				45				
Gln	Asp	Phe	Val	Leu	Leu	Glu	Asn	Phe	Thr	Ser	Glu	Ala	Ala	Phe	Ile
			50			55				60					
Gly	Asn	Leu	Arg	Arg	Arg	Phe	Arg	Glu	Asn	Leu	Ile	Tyr	Thr	Tyr	Ile
			65			70				75			80		
Gly	Pro	Val	Leu	Val	Ser	Val	Asn	Pro	Tyr	Arg	Asp	Leu	Gln	Ile	Tyr
				85			90				95				
Ser	Arg	Gln	His	Met	Glu	Arg	Tyr	Arg	Gly	Val	Ser	Phe	Tyr	Glu	Val
				100			105				110				
Pro	Pro	His	Leu	Phe	Ala	Val	Ala	Asp	Thr	Val	Tyr	Arg	Ala	Leu	Arg
				115			120				125				
Thr	Glu	Arg	Arg	Asp	Gln	Ala	Val	Met	Ile	Ser	Gly	Glu	Ser	Gly	Ala
				130			135				140				
Gly	Lys	Thr	Glu	Ala	Thr	Lys	Arg	Leu	Leu	Gln	Phe	Tyr	Ala	Glu	Thr

145	150	155	160
Cys Pro Ala Pro Glu Arg Gly Gly Ala Val Arg Asp Arg Leu Leu Gln			
165	170	175	
Ser Asn Pro Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Leu Arg Asn			
180	185	190	
Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met Asp Val Gln Phe Asp Phe			
195	200	205	
Lys Gly Ala Pro Val Gly Gly His Ile Leu Ser Tyr Pro Leu Glu Lys			
210	215	220	
Ser Arg Val Val His Gln Asn His Gly Glu Arg Asn Phe Thr Ser Ser			
225	230	235	240
Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg Leu Phe Ala Gly Trp Ala			
245	250	255	
Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr Trp			
260	265		

<210> 172

<211> 2650

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1216)

<400> 172

CTTTTGCTGC	TGCGCCGGGG	CAGGGGCTGC	CGGGGGCCCA	GGTCCCGCTT	CGAGACGGG	60
CGCGGTCCAG	GCGGGAGGCG	ACTCCCTAGG	AAGGGACCCG	GGGCGGGAGG	AGGAA ATG	118
					Met	
					1	

AGG CCG CGC GGA AGG AAG GCG GCG AGC CCC GGG GCC CCC CCG AGG CCT TGG	166		
Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro Trp			
5	10	15	

CCG CGT CAC AGC ACC CAC ATG GCC TCT GGA GTG GGC GCG GCC TTC GAG	214		
Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe Glu			
20	25	30	

GAA CTG CCT CAC GAC GGC ACG TGT GAC GAG TGC GAG CCC GAC GAG GCT	262		
Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala			
35	40	45	

CCG GGG GCC GAG GAA GTG TGC CGA GAA TGC GGC TTC TGC TAC TGC CGC	310		
Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg			
50	55	60	65

CGC CAT GCC GAG GCG CAC AGG CAG AAG TTC CTC AGT CAC CAT CTG GCC	358		
Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala			
70	75	80	

GAA TAC GTC CAC GGC TCC CAG GCC TGG ACC CCG CCA GCT GAC GGA GAG	406		
Glu Tyr Val His Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu			
85	90	95	

GGG GCG GGG AAG GAA GAA GCG GAG GTC AAG GTG GAG CAG GAG AGG GAG Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu 100 105 110	454
ATA GAA AGC GAG GCA GGG GAA GAG AGT GAG TCG GAG GAA GAG AGC GAG Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu 115 120 125	502
TCA GAG GAA GAG AGC GAG ACA GAG GAA GAG AGT GAG GAT GAG AGC GAT Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp 130 135 140 145	550
GAG GAG AGT GAA GAA GAC AGC GAG GAA GAA ATG GAG GAT GAG CAA GAA Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu 150 155 160	598
AGC GAG GCC GAA GAA GAC AAC CAA GAA GAA GGG GAA TCC GAG GCG GAG Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu 165 170 175	646
GGA GAA ACT GAG GCA GAA AGT GAA TTT GAC CCA GAA ATA GAA ATG GAA Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu 180 185 190	694
GCA GAG AGA GTG GCC AAG AGG AAG TGT CCG GAC CAT GGG CTT GAT TTG Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu 195 200 205	742
AGT ACC TAT TGC CAG GAA GAT AGG CAG CTC ATC TGT GTC CTG TGT CCA Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Cys Val Leu Cys Pro 210 215 220 225	790
GTC ATT GGG GCT CAC CAG GGC CAC CAA CTC TCC ACC CTA GAC GAA GCC Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala 230 235 240	838
TTT GAA GAA TTA AGA AGC AAA GAC TCA GGT GGA CTG AAG GCC GCT ATG Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met 245 250 255	886
ATC GAA TTG GTG GAA AGG TTG AAG TTC AAG AGC TCA GAC CCT AAA GTA Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val 260 265 270	934
ACT CGG GAC CAA ATG AAG ATG TTT ATA CAG CAG GAA TTT AAG AAA GTT Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val 275 280 285	982
CAG AAA GTG ATT GCT GAT GAG GAG CAG AAG GCC CTT CAT CTA GTG GAC Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp 290 295 300 305	1030
ATC CAA GAG GCA ATG GCC ACA GCT CAT GTG ACT GAG ATA CTG GCA GAC	1078

Ile Gln Glu Ala Met Ala Thr Ala His Val Thr Glu Ile Leu Ala Asp
 310 315 320

ATC CAA TCC CAC ATG GAT AGG TTG ATG ACT CAG ATG GCC CAA GCC AAG 1126
 Ile Gln Ser His Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys
 325 330 335

GAA CAA CTT GAT ACC TCT AAT GAA TCA GCT GAG CCA AAG GCA GAG GGC 1174
 Glu Gln Leu Asp Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly
 340 345 350

GAT GAG GAA GGA CCC AGT GGT GCC AGT GAA GAA GAG GAC ACA TGAAGGCTT 1225
 Asp Glu Glu Gly Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr
 355 360 365

GCTACCCCCA GTGGAAAATC ATCCCCTCCC CTTGTGTGTA TGTGACAGCG TGTATGTAAC 1285
 GGCTTCTGAT TTCTGTGAAA GCTGCTCAGC AACAAACGTA CTTCCACCAG ATGTGTCCCC 1345
 AGATCCACAG CAGGCACATA TCTCTCCAAG GGATGACCAG TTTATGCTT ACTGTGTGCT 1405
 TCTCATCCCC TGGTTGTGGT AGGTCAAGGA AAAGAGCCCC TTTGATCCAC CAGGAGCAAT 1465
 TAAGAAAGGT CCTTCAGGTA ATCCCCTCAAT GGCTGCTTTG AACTTACTCA GGAAAGCCAG 1525
 CCCCCATAAT ATTGTATTAC CAAACAGTAT CGCTTTGTTA GGAAGGATCT GGAATAATCT 1585
 TGAAGGGAAG TCAGAGTTT CTCCTGCCT ATTAACAAAA ACCCAATTGTT GTTCATATTG 1645
 AAGCATGAAA TAAATGAGAG CAAGGTAGGG CCAAATTAAAC TCTGTGGAC AGTCCCTAAA 1705
 AGTCCAGTTC TACATTGTG AAAATTGTGG TGCCATGAAT TAAGATGGAT GACTGGAAAA 1765
 AGGTGTTGGA GAAAGAGTTA AAGATGAGGA AGAGATATT TTAGTATATG AAGTTATCCA 1825
 GGACTTGATA TTCATAATTG AGTGCTGTGG AAATGAAAAA AATGATTGAA GAGGTGGAAC 1885
 GGAAATGACC TTAGGGGAA AAAAAGGAC CAAAGAAGTC TGATTAAAAG TTGAAATCAG 1945
 TATTCTGAA TTCAAATTGC TTGAATTTC CAAATAGTCA GTAAAGGATC TAATAGAAC 2005
 AGAATTATTG GGGTGAATTG TGAGGTTTT ATGGGCTTGT CACAACGTGA AGGGCTGGAA 2065
 TGTATATTAC CAAATGGGAA TTCCATTGT AGGTTTTGCT TAGTCCCACC CCCATTAG 2125
 CCTAATTGG CTAAACGCA GTATGGGAG AATTGTTCCC ATTCCATGTG TTCTGAATTG 2185
 AGCTCATCTC CCAGCATATA GATATATCCT CTTTAACTC CGACCAGAAC CCTTCTCCT 2245
 GTGGCACTCC CCACCCATAG ACCTTCAGAT CATCTCCCAC ACCCTGGATC TCACTCTCCT 2305
 CTTAGTAACA GAGACACTCC TGAGGTTGGA CTTCTTGCT TTTCTCTACT TCCAAATCAC 2365
 AATTCTTAC AACCAAGCTT TGTGCTCCCG AGTAAGCAGG GATGTACTAG GGGATGTAA 2425
 AACTGCAAAC TTAAAAACCT GCATCTCTT GAAGCATCAG TTTACTTAC CAAATGGTT 2485
 AGAGTCATAA GATGACCTAT TTTATATAA AAGTTATATT ATAGAATAAA ATGTTCATAC 2545
 GCATAGACTG TTAAG 2560

<210> 173

<211> 367

<212> PRT

<213> Homo sapiens

173

Met Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro

1 5 10 15

Trp Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe

20 25 30

Glu Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu

35 40 45

Ala Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys

50 55 60

Arg Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu

65	70	75	80												
Ala	Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly
85	90	95													
Glu	Gly	Ala	Gly	Lys	Glu	Glu	Ala	Glu	Val	Lys	Val	Glu	Gln	Glu	Arg
100	105	110													
Glu	Ile	Glu	Ser	Glu	Ala	Gly	Glu	Glu	Ser	Glu	Ser	Glu	Glu	Glu	Ser
115	120	125													
Glu	Ser	Glu	Glu	Ser	Glu	Thr	Glu	Glu	Glu	Ser	Glu	Asp	Glu	Ser	
130	135	140													
Asp	Glu	Glu	Ser	Glu	Glu	Asp	Ser	Glu	Glu	Glu	Met	Glu	Asp	Glu	Gln
145	150	155													160
Glu	Ser	Glu	Ala	Glu	Glu	Asp	Asn	Gln	Glu	Glu	Gly	Glu	Ser	Glu	Ala
165	170	175													
Glu	Gly	Glu	Thr	Glu	Ala	Glu	Ser	Glu	Phe	Asp	Pro	Glu	Ile	Glu	Met
180	185	190													
Glu	Ala	Glu	Arg	Val	Ala	Lys	Arg	Lys	Cys	Pro	Asp	His	Gly	Leu	Asp
195	200	205													
Leu	Ser	Thr	Tyr	Cys	Gln	Glu	Asp	Arg	Gln	Leu	Ile	Cys	Val	Leu	Cys
210	215	220													
Pro	Val	Ile	Gly	Ala	His	Gln	Gly	His	Gln	Leu	Ser	Thr	Leu	Asp	Glu
225	230	235													240
Ala	Phe	Glu	Glu	Leu	Arg	Ser	Lys	Asp	Ser	Gly	Gly	Leu	Lys	Ala	Ala
245	250	255													
Met	Ile	Glu	Leu	Val	Glu	Arg	Leu	Lys	Phe	Lys	Ser	Ser	Asp	Pro	Lys
260	265	270													
Val	Thr	Arg	Asp	Gln	Met	Lys	Met	Phe	Ile	Gln	Gln	Glu	Phe	Lys	Lys
275	280	285													
Val	Gln	Lys	Val	Ile	Ala	Asp	Glu	Glu	Gln	Lys	Ala	Leu	His	Leu	Val
290	295	300													
Asp	Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala
305	310	315													320
Asp	Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala
325	330	335													
Lys	Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu
340	345	350													
Gly	Asp	Glu	Glu	Gly	Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr	
355	360	365													

<210> 174

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 174

ttaagcttgc caccatgagc aaccccgagcg ccccacacc a

41

<210> 175

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 175

gtatcgattt aattgcgatc ccccatcag

29

176

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 176

cacctactgtatgacaccacattc

24

<210> 177

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 177

gagatgctgttccatgctggcttg

24

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 178

ggaaagctctccgtggctaacaag

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 179

catagtccttgacaagggtcacag

24

<210> 180

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 180

cccatcaccatcttccaggagc

22

<210> 181

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 181

ttcaccacccttttgtatgtcatcata

26

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06840

A. CLASSIFICATION OF SUBJECT MATTER

Int.Cl⁷ C12N15/12, C07K14/435, 16/18, C12P21/02,
 C12Q1/68, A61K38/00, 39/395, 48/00, A61P9/10,
 G01N33/50, 33/53,

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int.Cl⁷ C12N15/11-15/62, C07K14/00-14/825

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq,
 BIOSIS (DIALOG), WPI (DIALOG)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO, 99/14327, A2 (GENENTECH, INC.), 25 March, 1999 (25.03.99), especially, PRO246, FIG.26 (Accession No.X28436), FIG.27 (Accession No.Y05286) & AU, 9893121, A & ZA, 9808293, A	2,4,11,12, 36-40,43, 45,46
X	WO, 99/14328, A2 (GENENTECH, INC.), 25 March, 1999 (25.03.99), especially, FIGURE 16 (Accession No.X52221), FIGURE 17 (Accession No.Y13351) & ZA, 9808460, A & AU, 9893178, A & EP, 1027434, A2	2,4,11,12, 36-40,43, 45,46
X	US, 5942606, A (INCYTE PHARMACEUTICALS, INC.), 24 August, 1999 (24.08.99), especially, SEQ ID NO:2 (Accession No.X87000), SEQ ID NO:1 (Accession No.Y27096) (Family: none)	2,4,11,12, 36-40,43, 45,46
P,X	WO, 99/58660, A1 (HUMAN GENOME SCIENCES, INC.), 18 November, 1999 (18.11.99),	2,4,11,12, 36-40,43,

 Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search
 19 December, 2000 (19.12.00)Date of mailing of the international search report
 26 December, 2000 (26.12.00)Name and mailing address of the ISA/
 Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	especially, SEQ ID NO:39 (Accession No.Z65278), SEQ ID NO:291 (Accession No.Y76303) & AU, 9938831, A	45, 46
P, X	WO, 00/11015, A1 (ALPHAGENE, INC.), 02 March, 2000 (02.03.00), especially, SEQ ID NO:37 (Accession No.A23441), SEQ ID NO:38 (Accession No.Y94999) & AU, 9957847, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/15666, A2 (GENENTECH, INC.), 23 March, 2000 (23.03.00), especially, FIGURE 15 (Accession No.A30052), FIGURE 16 (Accession No.Y88574) & AU, 9958167, A	2, 4, 11, 12, 36-40, 43, 45, 46
A	TOPPER, James N. et al., "Blood flow and vascular gene expression: fluid shear stress as a modulator of endothelial phenotype", Molecular Medicine Today, January, 1999, Volume 5, Number 1, pages 40-46	1, 2, 4-12, 35-50
A	ANDO, Joji et al., "Flow-dependent Regulation of Gene Expression in Vascular Endothelial Cells", Japanese Heart Journal, January, 1996, Volume 37, Number 1, 19-32	1, 2, 4-12, 35-50

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06840

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: 22,33,51,57,66,69,76
because they relate to subject matter not required to be searched by this Authority, namely:

The inventions as set forth in claims 22, 33, 66 and 69 relate to "methods for inhibiting, promoting or controlling cell apoptosis". As stated in the description, these methods are performed for therapy in the human body. Therefore, these inventions pertain to methods for treatment of the human body by therapy. The inventions as set forth in claims 51, 57 and 76 relate to "drug delivery methods for inducing a fused antibody comprising an antibody bonded to a drug into arteriosclerotic focus" which are to be performed in the human body in therapy. Therefore, these inventions pertain to methods for treatment of the human body by therapy.
2. Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See extra sheet.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

The inventions as set forth in claims which relate to the base sequence represented by SEQ ID NO:143 or the amino acid sequence represented by SEQ ID NO:144

- Remark on Protest** The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

第Ⅰ欄1. の続き

薬剤とを結合させた融合抗体を動脈硬化巣へ誘導する「ドラッグデリバリー法」に関するものであり、ヒトを治療する際に体内で実施されるものであるから、人の身体の治療による処置方法に該当する。

第Ⅱ欄の続き

, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141,
1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 3
1, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57,
59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 8
5, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 10
9で表される塩基配列（若しくは、配列番号144, 146, 148, 150, 152, 1
54, 156, 158, 169, 171, 173, 112, 114, 118, 120, 12
2, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10,
12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 3
8, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64,
66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 9
2, 94, 96, 98, 100, 102, 104, 106, 108, 110で表されるアミ
ノ酸配列）、又は、配列番号115, 116, 129, 130, 131, 132, 133,
134で表される塩基配列、のそれぞれに関連した発明に共通する事項は、「血管内皮細胞
においてずり応力刺激により発現が誘導されるDNA」ということである。しかしながら、
「血管内皮細胞においてずり応力刺激により発現が誘導されるDNA」としては、出願人も
認識しているように endothelin-1 や monocyte chemotactic protein-1 などが既に公知で
あったから、請求の範囲に記載された上記各塩基配列（又は、アミノ酸配列）に関連した発
明に共通する「特別な技術的特徴」は存在しないといえる。

したがって、請求の範囲には、配列番号143, 145, 147, 149, 151, 15
3, 155, 157, 168, 170, 172, 111, 113, 117, 119, 12
1, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 1
1, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37,
39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 6
5, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91,
93, 95, 97, 99, 101, 103, 105, 107, 109で表される塩基配列
(若しくは、配列番号144, 146, 148, 150, 152, 154, 156, 15
8, 169, 171, 173, 112, 114, 118, 120, 122, 124, 12
6, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 1
6, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42,
44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 7
0, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96,
98, 100, 102, 104, 106, 108, 110で表されるアミノ酸配列）、又
は、配列番号115, 116, 129, 130, 131, 132, 133, 134で表され
る塩基配列、のそれぞれに関連した別異の86発明が含まれている。

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06840

Continuation of Box No.II of continuation of first sheet(1)

The requirement of unity of invention in international application (PCT Rule 13.1) is not satisfied unless there is a technical relationship between a group of inventions as set forth in claims involving one or more of the same or corresponding special technical feature. The term "special technical feature" means a technical feature clearly showing the contribution achieved by the inventions as set forth in the claims as a whole (PCT Rule 13.2). The requirement of unity of invention is judged without considering whether the group of inventions are described in separate claims or in a single claim in the alternative form (PCT Rule 13.3).

In the present case, the inventions relating to the base sequences represented by SEQ ID NOS: 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 and 109 (or the amino acid sequences represented by SEQ ID NOS: 144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108 and 110) or the base sequences represented by SEQ ID NO: 115, 116, 129, 130, 131, 132, 133 and 134 have a matter in common "DNA the expression of which is induced by a shear stress stimulus in hemoendothelial cells". However, there had been publicly known endothelin-1, monocyte chemotactic protein-1, etc. as "DNA the expression of which is induced by a shear stress stimulus in hemoendothelial cells", as the applicant recognizes. Therefore, it can be concluded that there is no "special technical feature" common to the inventions relating to the above-described base sequences (or amino acid sequences) as set forth in the claims.

Such being the case, the claims involve 86 separate inventions respectively relating to the base sequences represented by SEQ ID NOS: 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 and 109 (or the amino acid sequences represented by SEQ ID NOS: 144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108 and 110) or the base sequences represented by SEQ ID NO: 115, 116, 129, 130, 131, 132, 133 and 134.

A. 発明の属する分野の分類(国際特許分類(IPC))

Int. Cl' C12N15/12, C07K14/435, 16/18, C12P21/02,
 C12Q1/68, A61K38/00, 39/395, 48/00, A61P9/10,
 G01N33/50, 33/53,

B. 調査を行った分野

調査を行った最小限資料(国際特許分類(IPC))

Int. Cl' C12N15/11-15/62, C07K14/00-14/825

最小限資料以外の資料で調査を行った分野に含まれるもの

国際調査で使用した電子データベース(データベースの名称、調査に使用した用語)

GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq,
 BIOSIS(DIALOG), WPI(DIALOG)

C. 関連すると認められる文献

引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
X	WO, 99/14327, A2 (GENENTECH, INC.) 25.3月.1999 (25.03.99) 特に、PRO246, FIG. 26(Accession No. X28436), FIG. 27(Accession No. Y05286) & AU, 9893121, A & ZA, 9808293, A	2, 4, 11, 12, 36-40, 43, 45, 46
X	WO, 99/14328, A2 (GENENTECH, INC.) 25.3月.1999 (25.03.99) 特に、FIGURE 16(Accession No. X52221),	2, 4, 11, 12, 36-40, 43, 45, 46

 C欄の続きにも文献が列挙されている。 パテントファミリーに関する別紙を参照。

* 引用文献のカテゴリー

「A」特に関連のある文献ではなく、一般的技術水準を示すもの

「E」国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの

「L」優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献(理由を付す)

「O」口頭による開示、使用、展示等に言及する文献

「P」国際出願日前で、かつ優先権の主張の基礎となる出願

の日の後に公表された文献

「T」国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの

「X」特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの

「Y」特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの

「&」同一パテントファミリー文献

国際調査を完了した日 19.12.00	国際調査報告の発送日 26.12.00
国際調査機関の名称及びあて先 日本国特許庁 (ISA/JP) 郵便番号 100-8915 東京都千代田区霞が関三丁目4番3号	特許庁審査官(権限のある職員) 内田俊生 電話番号 03-3581-1101 内線 3488 4N 8214

C(続き) 関連すると認められる文献		関連する 請求の範囲の番号
引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	
X	FIGURE 17(Accession No. Y13351) & ZA, 9808460, A & AU, 9893178, A & EP, 1027434, A2	
X	US, 5942606, A (INCYTE PHARMACEUTICALS, INC.) 24.8月.1999 (24.08.99) 特に、SEQ ID NO:2(Accession No. X87000), SEQ ID NO:1(Accession No. Y27096) (ファミリーなし)	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 99/58660, A1 (HUMAN GENOME SCIENCES, INC.) 18.11月.1999 (18.11.99) 特に、SEQ ID NO:39(Accession No. Z65278), SEQ ID NO:291(Accession No. Y76303) & AU, 9938831, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/11015, A1 (ALPHAGENE, INC.) 2.3月.2000 (02.03.00) 特に、SEQ ID NO:37(Accession No. A23441), SEQ ID NO:38(Accession No. Y94999) & AU, 9957847, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/15666, A2 (GENENTECH, INC.) 23.3月.2000 (23.03.00) 特に、FIGURE 15(Accession No. A30052), FIGURE 16(Accession No. Y88574) & AU, 9958167, A	2, 4, 11, 12, 36-40, 43, 45, 46
A	TOPPER, James N. et al., "Blood flow and vascular gene expression: fluid shear stress as a modulator of endothelial phenotype", Molecular Medicine Today, January, 1999, Volume 5, Number 1, pages 40-46	1, 2, 4-12, 35-50
A	ANDO, Joji et al., "Flow-dependent Regulation of Gene Expression in Vascular Endothelial Cells", Japanese Heart Journal, January, 1996, Volume 37, Number 1, 19-32	1, 2, 4-12, 35-50

第I欄 請求の範囲の一部の調査ができないときの意見（第1ページの2の続き）

法第8条第3項（PCT17条(2)(a)）の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

1. 請求の範囲 22, 33, 51, 57, 66, 69, 76 は、この国際調査機関が調査をすることを要しない対象に係るものである。つまり、
請求の範囲 22, 33, 66, 69 の発明は「細胞のアポトーシスを抑制、促進または調節する方法」に関するものであるが、明細書にも記載されているように、これらはヒトの体内で治療を目的として実施されるものであるから、これらの発明は人の身体の治療による処置方法に該当する。また、請求の範囲 51, 57, 76 の発明は、「抗体と
2. 請求の範囲 _____ は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、
3. 請求の範囲 _____ は、従属請求の範囲であって PCT 規則 6.4(a) の第 2 文及び第 3 文の規定に従って記載されていない。

第II欄 発明の単一性が欠如しているときの意見（第1ページの3の続き）

次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

国際出願における発明の単一性の要件（PCT 規則 13.1）は、請求の範囲に記載された一群の発明の間に一又は二以上の同一又は対応する特別な技術的特徴を含む技術的関係があるときに限り、満たされるものであって、この「特別な技術的特徴」とは、請求の範囲に記載された各発明が全体として先行技術に対して行う貢献を明示する技術的特徴のことである（PCT 規則 13.2）。また、発明の単一性の要件の判断は、一群の発明が別個の請求の範囲に記載されているか単一の請求の範囲に併せて記載されているかを考慮することなく行われる（PCT 規則 13.3）。

そこで、請求の範囲をみると、請求の範囲に記載された配列番号 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113

1. 出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求の範囲について作成した。
2. 追加調査手数料を要求するまでもなく、すべての調査可能な請求の範囲について調査することができたので、追加調査手数料の納付を求めなかった。
3. 出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったので、この国際調査報告は、手数料の納付のあった次の請求の範囲のみについて作成した。
4. 出願人が必要な追加調査手数料を期間内に納付しなかったので、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求の範囲について作成した。

請求の範囲中の配列番号 143 で表される塩基配列又は配列番号 144 で表されるアミノ酸配列に関連した発明

追加調査手数料の異議の申立てに関する注意

- 追加調査手数料の納付と共に出願人から異議申立てがあった。
- 追加調査手数料の納付と共に出願人から異議申立てがなかった。